

C 253	21	0.3	24	1	AZ404871	ACCESSION:AZ404871	326	20.4	0.3	22	1	CF310366	ACCESSION:CF310366
C 254	21	0.3	24	1	AZ786257	ACCESSION:AZ786257	327	20.4	0.3	22	1	CF311269	ACCESSION:CF311269
C 255	21	0.3	25	1	N27663	ACCESSION:N27663	C 328	20.4	0.3	22	1	CF311713	ACCESSION:CF311713
C 256	21	0.3	25	1	CG726337	ACCESSION:CG726337	C 329	20.4	0.3	22	1	CF312498	ACCESSION:CF312498
C 257	21	0.3	26	1	CF280688	ACCESSION:CF280688	C 330	20.4	0.3	22	1	CF330679	ACCESSION:CF330679
C 258	21	0.3	27	1	CF310745	ACCESSION:CF310745	C 331	20.4	0.3	22	1	CF333430	ACCESSION:CF333430
C 259	21	0.3	29	1	CF295451	ACCESSION:CF295451	C 332	20.4	0.3	22	1	CF334781	ACCESSION:CF334781
C 260	21	0.3	29	1	CF299155	ACCESSION:CF299155	C 333	20.4	0.3	22	1	CF336250	ACCESSION:CF336250
C 261	21	0.3	29	1	CF314795	ACCESSION:CF314795	C 334	20.4	0.3	22	1	CF337580	ACCESSION:CF337580
C 262	21	0.3	30	1	BQ592535	ACCESSION:BQ592535	C 335	20.4	0.3	22	1	CF338524	ACCESSION:CF338524
C 263	21	0.3	30	1	TA226050P	ACCESSION:AL480085	C 336	20.4	0.3	22	1	A2310066	ACCESSION:AZ310066
C 264	21	0.3	31	1	CF311684	ACCESSION:CF311684	C 337	20.4	0.3	22	1	A2351527	ACCESSION:AZ351527
C 265	21	0.3	31	1	CF312835	ACCESSION:CF312835	C 338	20.4	0.3	22	1	A2357630	ACCESSION:AZ357630
C 266	21	0.3	32	1	AV675687	ACCESSION:AV675687	C 339	20.4	0.3	22	1	A2374487	ACCESSION:AZ374487
C 267	21	0.3	32	1	AV965254	ACCESSION:AV965254	C 340	20.4	0.3	22	1	A2388103	ACCESSION:AZ388103
C 268	21	0.3	32	1	AV965452	ACCESSION:AV965452	C 341	20.4	0.3	22	1	A2401908	ACCESSION:AZ401908
C 269	21	0.3	32	1	BX551100	ACCESSION:BX551100	C 342	20.4	0.3	22	1	A2424307	ACCESSION:AZ424307
C 270	21	0.3	32	1	AX555525	ACCESSION:BX555525	C 343	20.4	0.3	22	1	A2428818	ACCESSION:AZ428818
C 271	21	0.3	32	1	AX557354	ACCESSION:BX557354	C 344	20.4	0.3	22	1	A2459654	ACCESSION:AZ459654
C 272	20.8	0.3	24	1	BG70391	ACCESSION:BG70391	C 345	20.4	0.3	22	1	A2463503	ACCESSION:AZ463503
C 273	20.8	0.3	24	1	AX554611	ACCESSION:BX554611	C 346	20.4	0.3	22	1	A2463652	ACCESSION:AZ463652
C 274	20.8	0.3	24	1	CA853764	ACCESSION:CA853764	C 347	20.4	0.3	22	1	A2582403	ACCESSION:AZ582403
C 275	20.8	0.3	24	1	CF276855	ACCESSION:CF276855	C 348	20.4	0.3	22	1	A2607658	ACCESSION:AZ607658
C 276	20.8	0.3	24	1	CF301361	ACCESSION:CF301361	C 349	20.4	0.3	22	1	A2654691	ACCESSION:AZ654691
C 277	20.8	0.3	24	1	CF312319	ACCESSION:CF312319	C 350	20.4	0.3	22	1	A2760533	ACCESSION:AZ760533
C 278	20.8	0.3	24	1	CF320862	ACCESSION:CF320862	C 351	20.4	0.3	22	1	A2779844	ACCESSION:AZ779844
C 279	20.8	0.3	24	1	A2328848	ACCESSION:AZ328848	C 352	20.4	0.3	22	1	A2785019	ACCESSION:AZ785019
C 280	20.8	0.3	24	1	A2363562	ACCESSION:AZ363562	C 353	20.4	0.3	22	1	A2787098	ACCESSION:AZ787098
C 281	20.8	0.3	24	1	A2386491	ACCESSION:AZ386491	C 354	20.4	0.3	22	1	A2787606	ACCESSION:AZ787606
C 282	20.8	0.3	24	1	A2390642	ACCESSION:AZ390642	C 355	20.4	0.3	22	1	A2792704	ACCESSION:AZ792704
C 283	20.8	0.3	24	1	A2459280	ACCESSION:AZ459280	C 356	20.4	0.3	22	1	A2810674	ACCESSION:AZ810674
C 284	20.8	0.3	24	1	A2644621	ACCESSION:AZ644621	C 357	20.4	0.3	22	1	A2820439	ACCESSION:AZ820439
C 285	20.8	0.3	24	1	A2833490	ACCESSION:AZ833490	C 358	20.4	0.3	22	1	A2841661	ACCESSION:AZ841661
C 286	20.8	0.3	24	1	A2970038	ACCESSION:AZ970038	C 359	20.4	0.3	22	1	A2843514	ACCESSION:AZ843514
C 287	20.8	0.3	24	1	A2984490	ACCESSION:AZ984490	C 360	20.4	0.3	22	1	A2946102	ACCESSION:AZ946102
C 288	20.8	0.3	24	1	A2993423	ACCESSION:AZ993423	C 361	20.4	0.3	22	1	TA131B09P	ACCESSION:AL464164
C 289	20.8	0.3	24	1	TA169D12P	ACCESSION:AL478922	C 362	20.4	0.3	22	1	TA1329F10P	ACCESSION:AL492691
C 290	20.8	0.3	24	1	TA27B08Q	ACCESSION:AL453584	C 363	20.4	0.3	22	1	TA35C12Q	ACCESSION:AL454556
C 291	20.8	0.3	24	1	TA354C06P	ACCESSION:AL494439	C 364	20.4	0.3	22	1	TA380A07P	ACCESSION:AL497713
C 292	20.8	0.3	24	1	TA371F11P	ACCESSION:AL495622	C 365	20.4	0.3	23	1	AL048745	ACCESSION:AL048745
C 293	20.8	0.3	24	1	TA95B08P	ACCESSION:AL459003	C 366	20.4	0.3	23	1	CF279238	ACCESSION:CF279238
C 294	20.8	0.3	25	1	AL587648	ACCESSION:AL587648	C 367	20.4	0.3	23	1	CF297943	ACCESSION:CF297943
C 295	20.8	0.3	25	1	N33150	ACCESSION:N33150	C 368	20.4	0.3	23	1	CF310501	ACCESSION:CF310501
C 296	20.8	0.3	25	1	A2381039	ACCESSION:AZ381039	C 369	20.4	0.3	23	1	CF319212	ACCESSION:CF319212
C 297	20.8	0.3	25	1	A2386891	ACCESSION:AZ386891	C 370	20.4	0.3	23	1	CF322953	ACCESSION:CF322953
C 298	20.8	0.3	25	1	TA154D03P	ACCESSION:AL472971	C 371	20.4	0.3	23	1	CF329042	ACCESSION:CF329042
C 299	20.8	0.3	26	1	CF336199	ACCESSION:CF336199	C 372	20.4	0.3	23	1	CF334657	ACCESSION:CF334657
C 300	20.8	0.3	27	1	CF639306	ACCESSION:CF639306	C 373	20.4	0.3	23	1	A2309219	ACCESSION:AZ309219
C 301	20.8	0.3	27	1	TA257B07P	ACCESSION:AL483278	C 374	20.4	0.3	23	1	A2309851	ACCESSION:AZ309851
C 302	20.8	0.3	28	1	AU257468	ACCESSION:AU257468	C 375	20.4	0.3	23	1	A2311314	ACCESSION:AZ311314
C 303	20.8	0.3	28	1	CF277114	ACCESSION:CF277114	C 376	20.4	0.3	23	1	A23113922	ACCESSION:AZ3113922
C 304	20.8	0.3	28	1	CF299294	ACCESSION:CF299294	C 377	20.4	0.3	23	1	A2351354	ACCESSION:AZ351354
C 305	20.8	0.3	28	1	T56352	ACCESSION:T56352	C 378	20.4	0.3	23	1	A2357645	ACCESSION:AZ357645
C 306	20.8	0.3	29	1	AX568640	ACCESSION:BX568640	C 379	20.4	0.3	23	1	A2419236	ACCESSION:AZ419236
C 307	20.8	0.3	29	1	CF328476	ACCESSION:CF328476	C 380	20.4	0.3	23	1	A2465327	ACCESSION:AZ465327
C 308	20.8	0.3	30	1	DR31A15T	ACCESSION:AL987581	C 381	20.4	0.3	23	1	AZ481702	ACCESSION:AZ481702
C 309	20.8	0.3	30	1	TA247F06P	ACCESSION:AL483252	C 382	20.4	0.3	23	1	AZ588254	ACCESSION:AZ588254
C 310	20.8	0.3	31	1	A2435998	ACCESSION:AZ435998	C 383	20.4	0.3	23	1	AZ593540	ACCESSION:AZ593540
C 311	20.8	0.3	32	1	AX568999	ACCESSION:AX568999	C 384	20.4	0.3	23	1	AZ610785	ACCESSION:AZ610785
C 312	20.8	0.3	32	1	TA296152	ACCESSION:CF296152	C 385	20.4	0.3	23	1	AZ621676	ACCESSION:AZ621676
C 313	20.8	0.3	32	1	A2345558	ACCESSION:AZ345558	C 386	20.4	0.3	23	1	AZ647637	ACCESSION:AZ647637
C 314	20.8	0.3	32	1	CG707472	ACCESSION:CG707472	C 387	20.4	0.3	23	1	AZ654903	ACCESSION:AZ654903
C 315	20.6	0.3	28	1	CF334115	ACCESSION:CF334115	C 388	20.4	0.3	23	1	AZ778751	ACCESSION:AZ778751
C 316	20.6	0.3	29	1	CF300706	ACCESSION:CF300706	C 389	20.4	0.3	23	1	AZ787184	ACCESSION:AZ787184
C 317	20.6	0.3	29	1	CF330960	ACCESSION:CF330960	C 390	20.4	0.3	23	1	AZ792751	ACCESSION:AZ792751
C 318	20.6	0.3	30	1	AX555986	ACCESSION:BX555986	C 391	20.4	0.3	23	1	AZ801003	ACCESSION:AZ801003
C 319	20.6	0.3	30	1	AX554037	ACCESSION:BX554037	C 392	20.4	0.3	23	1	AZ817623	ACCESSION:AZ817623
C 320	20.6	0.3	31	1	AX554615	ACCESSION:BX554615	C 393	20.4	0.3	23	1	AZ859570	ACCESSION:AZ859570
C 321	20.6	0.3	31	1	AX556269	ACCESSION:BX556269	C 394	20.4	0.3	23	1	AZ939608	ACCESSION:AZ939608
C 322	20.4	0.3	22	1	AX332181	ACCESSION:AX332181	C 395	20.4	0.3	23	1	BH000534	ACCESSION:BH000534
C 323	20.4	0.3	22	1	AW332399	ACCESSION:AW332399	C 396	20.4	0.3	23	1	TA151C02Q	ACCESSION:AL473028
C 324	20.4	0.3	22	1	CF299342	ACCESSION:CF299342	C 397	20.4	0.3	23	1	TA274B03P	ACCESSION:AL484584
C 325	20.4	0.3	22	1	CF300133	ACCESSION:CF300133	C 398	20.4	0.3	23	1		

C 399	20.4	0.3	23	1	TA353A10P	ACCESSION: AL494456	472	20	0.3	20	1	T50579	ACCESSION: T50579
C 400	20.4	0.3	24	1	AZ438069	ACCESSION: AZ438069	473	20	0.3	20	1	AZ307671	ACCESSION: AZ307671
C 401	20.4	0.3	25	1	CF317007	ACCESSION: CF317007	474	20	0.3	20	1	AZ333980	ACCESSION: AZ333980
C 402	20.4	0.3	26	1	CF299646	ACCESSION: CF299646	C 475	20	0.3	20	1	AZ341530	ACCESSION: AZ341530
C 403	20.4	0.3	26	1	R26779	ACCESSION: R26779	C 476	20	0.3	20	1	AZ343031	ACCESSION: AZ343031
C 404	20.4	0.3	26	1	CNS00BGV	ACCESSION: AL057060	C 477	20	0.3	20	1	AZ345856	ACCESSION: AZ345856
C 405	20.4	0.3	26	1	TA321G11P	ACCESSION: AL492371	C 478	20	0.3	20	1	AZ351273	ACCESSION: AZ351273
C 406	20.4	0.3	27	1	N34459	ACCESSION: N34459	C 479	20	0.3	20	1	AZ357623	ACCESSION: AZ357623
C 407	20.4	0.3	27	1	T52979	ACCESSION: T52979	C 480	20	0.3	20	1	AZ369734	ACCESSION: AZ369734
C 408	20.4	0.3	27	1	AZ812708	ACCESSION: AZ812708	C 481	20	0.3	20	1	AZ386573	ACCESSION: AZ386573
C 409	20.4	0.3	28	1	AZ357605	ACCESSION: AZ357605	C 482	20	0.3	20	1	AZ396481	ACCESSION: AZ396481
C 410	20.4	0.3	29	1	AL048747	ACCESSION: AL048747	C 483	20	0.3	20	1	AZ442328	ACCESSION: AZ442328
C 411	20.4	0.3	29	1	BQ586486	ACCESSION: BQ586486	C 484	20	0.3	20	1	AZ463331	ACCESSION: AZ463331
C 412	20.4	0.3	29	1	BX567540	ACCESSION: BX567540	C 485	20	0.3	20	1	AZ477734	ACCESSION: AZ477734
C 413	20.4	0.3	29	1	BX627582	ACCESSION: BX627582	C 486	20	0.3	20	1	AZ479464	ACCESSION: AZ479464
C 414	20.4	0.3	29	1	CF312595	ACCESSION: CF312595	C 487	20	0.3	20	1	AZ498625	ACCESSION: AZ498625
C 415	20.4	0.3	29	1	AZ825156	ACCESSION: AZ825156	C 488	20	0.3	20	1	AZ514729	ACCESSION: AZ514729
C 416	20.4	0.3	29	1	TA378G07P	ACCESSION: AL497621	C 489	20	0.3	20	1	AZ579178	ACCESSION: AZ579178
C 417	20.4	0.3	30	1	BE539470	ACCESSION: BE539470	C 490	20	0.3	20	1	AZ581208	ACCESSION: AZ581208
C 418	20.4	0.3	30	1	BM280395	ACCESSION: BM280395	C 491	20	0.3	20	1	AZ588011	ACCESSION: AZ588011
C 419	20.4	0.3	30	1	BX549675	ACCESSION: BX549675	C 492	20	0.3	20	1	AZ607328	ACCESSION: AZ607328
C 420	20.4	0.3	30	1	BX551003	ACCESSION: BX551003	C 493	20	0.3	20	1	AZ623155	ACCESSION: AZ623155
C 421	20.4	0.3	30	1	BX554779	ACCESSION: BX554779	C 494	20	0.3	20	1	AZ623214	ACCESSION: AZ623214
C 422	20.4	0.3	30	1	BX555710	ACCESSION: BX555710	C 495	20	0.3	20	1	AZ643992	ACCESSION: AZ643992
C 423	20.4	0.3	30	1	BX559425	ACCESSION: BX559425	C 496	20	0.3	20	1	AZ645829	ACCESSION: AZ645829
C 424	20.4	0.3	30	1	BX563547	ACCESSION: BX563547	C 497	20	0.3	20	1	AZ650271	ACCESSION: AZ650271
C 425	20.4	0.3	30	1	BX565972	ACCESSION: BX565972	C 498	20	0.3	20	1	AZ760838	ACCESSION: AZ760838
C 426	20.4	0.3	31	1	AW245279	ACCESSION: AW245279	C 499	20	0.3	20	1	AZ764504	ACCESSION: AZ764504
C 427	20.4	0.3	31	1	BX554068	ACCESSION: BX554068	C 500	20	0.3	20	1	AZ765211	ACCESSION: AZ765211
C 428	20.4	0.3	31	1	BX557470	ACCESSION: BX557470	C 501	20	0.3	20	1	AZ772091	ACCESSION: AZ772091
C 429	20.4	0.3	31	1	BX558479	ACCESSION: BX558479	C 502	20	0.3	20	1	AZ779425	ACCESSION: AZ779425
C 430	20.4	0.3	31	1	BX559254	ACCESSION: BX559254	C 503	20	0.3	20	1	AZ784041	ACCESSION: AZ784041
C 431	20.4	0.3	32	1	CF296152	ACCESSION: CF296152	C 504	20	0.3	20	1	AZ793467	ACCESSION: AZ793467
C 432	20.2	0.3	25	1	AU265663	ACCESSION: AU265663	C 505	20	0.3	20	1	AZ798529	ACCESSION: AZ798529
C 433	20.2	0.3	25	1	CF317378	ACCESSION: CF317378	C 506	20	0.3	20	1	AZ805163	ACCESSION: AZ805163
C 434	20.2	0.3	25	1	AZ404078	ACCESSION: AZ404078	C 507	20	0.3	20	1	AZ806521	ACCESSION: AZ806521
C 435	20.2	0.3	26	1	AZ316353	ACCESSION: AZ316353	C 508	20	0.3	20	1	AZ806585	ACCESSION: AZ806585
C 436	20.2	0.3	26	1	AZ355083	ACCESSION: AZ355083	C 509	20	0.3	20	1	AZ809306	ACCESSION: AZ809306
C 437	20.2	0.3	26	1	AZ623156	ACCESSION: AZ623156	C 510	20	0.3	20	1	AZ810986	ACCESSION: AZ810986
C 438	20.2	0.3	26	1	AZ635695	ACCESSION: AZ635695	C 511	20	0.3	20	1	AZ813908	ACCESSION: AZ813908
C 439	20.2	0.3	27	1	CF298133	ACCESSION: CF298133	C 512	20	0.3	20	1	AZ817323	ACCESSION: AZ817323
C 440	20.2	0.3	27	1	AZ434285	ACCESSION: AZ434285	C 513	20	0.3	20	1	AZ817414	ACCESSION: AZ817414
C 441	20.2	0.3	27	1	AZ458228	ACCESSION: AZ458228	C 514	20	0.3	20	1	AZ817467	ACCESSION: AZ817467
C 442	20.2	0.3	28	1	AL587605	ACCESSION: AL587605	C 515	20	0.3	20	1	AZ817608	ACCESSION: AZ817608
C 443	20.2	0.3	28	1	AW332443	ACCESSION: AW332443	C 516	20	0.3	20	1	AZ818489	ACCESSION: AZ818489
C 444	20.2	0.3	28	1	CF307749	ACCESSION: CF307749	C 517	20	0.3	20	1	AZ818816	ACCESSION: AZ818816
C 445	20.2	0.3	28	1	AZ836072	ACCESSION: AZ836072	C 518	20	0.3	20	1	AZ837491	ACCESSION: AZ837491
C 446	20.2	0.3	28	1	TA29A09P	ACCESSION: AL453073	C 519	20	0.3	20	1	AZ841342	ACCESSION: AZ841342
C 447	20.2	0.3	29	1	BQ583967	ACCESSION: BQ583967	C 520	20	0.3	20	1	AZ841558	ACCESSION: AZ841558
C 448	20.2	0.3	29	1	AZ827060	ACCESSION: AZ827060	C 521	20	0.3	20	1	AZ858052	ACCESSION: AZ858052
C 449	20.2	0.3	30	1	BX659426	ACCESSION: BX659426	C 522	20	0.3	20	1	AZ936914	ACCESSION: AZ936914
C 450	20.2	0.3	31	1	AU268044	ACCESSION: AU268044	C 523	20	0.3	20	1	AZ945180	ACCESSION: AZ945180
C 451	20.2	0.3	31	1	BQ591372	ACCESSION: BQ591372	C 524	20	0.3	20	1	AZ963973	ACCESSION: AZ963973
C 452	20.2	0.3	31	1	CF297930	ACCESSION: CF297930	C 525	20	0.3	21	1	AL048777	ACCESSION: AL048777
C 453	20.2	0.3	31	1	AZ486763	ACCESSION: AZ486763	C 526	20	0.3	21	1	BX556006	ACCESSION: BX556006
C 454	20.2	0.3	31	1	AZ785111	ACCESSION: AZ785111	C 527	20	0.3	21	1	BX558161	ACCESSION: BX558161
C 455	20.2	0.3	31	1	AW334823	ACCESSION: AW334823	C 528	20	0.3	21	1	CF276638	ACCESSION: CF276638
C 456	20.2	0.3	32	1	CF280913	ACCESSION: CF280913	C 529	20	0.3	21	1	CF282216	ACCESSION: CF282216
C 457	20.2	0.3	20	1	CF280235	ACCESSION: CF280235	C 530	20	0.3	21	1	CF292703	ACCESSION: CF292703
C 458	20.2	0.3	20	1	CF282414	ACCESSION: CF282414	C 531	20	0.3	21	1	CF295642	ACCESSION: CF295642
C 459	20.2	0.3	20	1	CF299822	ACCESSION: CF299822	C 532	20	0.3	21	1	CF297615	ACCESSION: CF297615
C 460	20.2	0.3	20	1	CF301720	ACCESSION: CF301720	C 533	20	0.3	21	1	CF298322	ACCESSION: CF298322
C 461	20.2	0.3	20	1	CF302027	ACCESSION: CF302027	C 534	20	0.3	21	1	CF300809	ACCESSION: CF300809
C 462	20.2	0.3	20	1	CF310604	ACCESSION: CF310604	C 535	20	0.3	21	1	CF312715	ACCESSION: CF312715
C 463	20.2	0.3	20	1	CF313067	ACCESSION: CF313067	C 536	20	0.3	21	1	CF316073	ACCESSION: CF316073
C 464	20.2	0.3	20	1	CF313569	ACCESSION: CF313569	C 537	20	0.3	21	1	CF326952	ACCESSION: CF326952
C 465	20.2	0.3	20	1	CF319133	ACCESSION: CF319133	C 538	20	0.3	21	1	CF327391	ACCESSION: CF327391
C 466	20.2	0.3	20	1	CF321721	ACCESSION: CF321721	C 539	20	0.3	21	1	CF332956	ACCESSION: CF332956
C 467	20.2	0.3	20	1	CF328565	ACCESSION: CF328565	C 540	20	0.3	21	1	CF338057	ACCESSION: CF338057
C 468	20.2	0.3	20	1	CF333173	ACCESSION: CF333173	C 541	20	0.3	21	1	CF338522	ACCESSION: CF338522
C 469	20.2	0.3	20	1	CF334170	ACCESSION: CF334170	C 542	20	0.3	21	1	AZ348593	ACCESSION: AZ348593
C 470	20.2	0.3	20	1	CF336525	ACCESSION: CF336525	C 543	20	0.3	21	1	AZ350611	ACCESSION: AZ350611
C 471	20.2	0.3	20	1	CF337494	ACCESSION: CF337494	C 544	20	0.3	21	1	AZ386711	ACCESSION: AZ386711

C 691	19	0.3	19	1	AZ307313	ACCSSION:AZ307313	C 764	19	0.3	22	1	TA231E08Q	ACCSSION:AL480935
C 692	19	0.3	19	1	AZ310079	ACCSSION:AZ310079	C 765	19	0.3	26	1	CF318508	ACCSSION:CF318508
C 693	19	0.3	19	1	AZ310105	ACCSSION:AZ310105	C 766	19	0.3	26	1	TA236D08P	ACCSSION:AL482943
C 694	19	0.3	19	1	AZ317743	ACCSSION:AZ317743	C 767	19	0.3	27	1	BI094728	ACCSSION:BI094728
C 695	19	0.3	19	1	AZ340311	ACCSSION:AZ340311	768	19	0.3	27	1	CF311022	ACCSSION:CF311022
C 696	19	0.3	19	1	AZ350519	ACCSSION:AZ350519	769	19	0.3	27	1	NS1845	ACCSSION:NS1845
C 697	19	0.3	19	1	AZ364226	ACCSSION:AZ364226	770	19	0.3	27	1	TA386G03Q	ACCSSION:AL498287
C 698	19	0.3	19	1	AZ356696	ACCSSION:AZ356696	C 771	19	0.3	28	1	AI971979	ACCSSION:AI971979
C 699	19	0.3	19	1	AZ374409	ACCSSION:AZ374409	C 772	19	0.3	28	1	AZ803177	ACCSSION:AZ803177
C 700	19	0.3	19	1	AZ374619	ACCSSION:AZ374619	C 773	19	0.3	28	1	TA173D10P	ACCSSION:AL473898
C 701	19	0.3	19	1	AZ385952	ACCSSION:AZ385952	774	19	0.3	28	1	TA327D04P	ACCSSION:AL497297
C 702	19	0.3	19	1	AZ391509	ACCSSION:AZ391509	775	19	0.3	29	1	BX561329	ACCSSION:BX561329
C 703	19	0.3	19	1	AZ410050	ACCSSION:AZ410050	C 776	19	0.3	29	1	CF310757	ACCSSION:CF310757
C 704	19	0.3	19	1	AZ414413	ACCSSION:AZ414413	C 777	18.8	0.3	22	1	CF298427	ACCSSION:CF298427
C 705	19	0.3	19	1	AZ422604	ACCSSION:AZ422604	C 778	18.8	0.3	22	1	TA303G05P	ACCSSION:AL497383
C 706	19	0.3	19	1	AZ424716	ACCSSION:AZ424716	779	18.8	0.3	23	1	BM568055	ACCSSION:BM568055
C 707	19	0.3	19	1	AZ441329	ACCSSION:AZ441329	780	18.8	0.3	23	1	CF290997	ACCSSION:CF290997
C 708	19	0.3	19	1	AZ442365	ACCSSION:AZ442365	781	18.8	0.3	23	1	CF311534	ACCSSION:CF311534
C 709	19	0.3	19	1	AZ453930	ACCSSION:AZ453930	C 782	18.8	0.3	23	1	AZ382013	ACCSSION:AZ382013
C 710	19	0.3	19	1	AZ460906	ACCSSION:AZ460906	C 783	18.8	0.3	23	1	AZ486853	ACCSSION:AZ486853
C 711	19	0.3	19	1	AZ471494	ACCSSION:AZ471494	784	18.8	0.3	23	1	AZ627841	ACCSSION:AZ627841
C 712	19	0.3	19	1	AZ476576	ACCSSION:AZ476576	785	18.8	0.3	23	1	AZ645254	ACCSSION:AZ645254
C 713	19	0.3	19	1	AZ486786	ACCSSION:AZ486786	C 786	18.8	0.3	23	1	TA55C06P	ACCSSION:AL455778
C 714	19	0.3	19	1	AZ490652	ACCSSION:AZ490652	C 787	18.8	0.3	25	1	AZ867155	ACCSSION:AZ867155
C 715	19	0.3	19	1	AZ508040	ACCSSION:AZ508040	C 788	18.8	0.3	27	1	BM555323	ACCSSION:BM555323
C 716	19	0.3	19	1	AZ579119	ACCSSION:AZ579119	C 789	18.8	0.3	30	1	TA247F06P	ACCSSION:AL483252
C 717	19	0.3	19	1	AZ583970	ACCSSION:AZ583970	C 790	18.6	0.2	25	1	AW312788	ACCSSION:AW312788
C 718	19	0.3	19	1	AZ585865	ACCSSION:AZ585865	791	18.6	0.2	25	1	AW249476	ACCSSION:AW249476
C 719	19	0.3	19	1	AZ593210	ACCSSION:AZ593210	792	18.6	0.2	25	1	CF319953	ACCSSION:CF319953
C 720	19	0.3	19	1	AZ616154	ACCSSION:AZ616154	C 793	18.6	0.2	25	1	AZ442170	ACCSSION:AZ442170
C 721	19	0.3	19	1	AZ627844	ACCSSION:AZ627844	C 794	18.6	0.2	25	1	AZ476141	ACCSSION:AZ476141
C 722	19	0.3	19	1	AZ631701	ACCSSION:AZ631701	795	18.6	0.2	25	1	BZ765670	ACCSSION:BZ765670
C 723	19	0.3	19	1	AZ633821	ACCSSION:AZ633821	796	18.6	0.2	26	1	BM658913	ACCSSION:BM658913
C 724	19	0.3	19	1	AZ643659	ACCSSION:AZ643659	797	18.6	0.2	26	1	BM563414	ACCSSION:BM563414
C 725	19	0.3	19	1	AZ644698	ACCSSION:AZ644698	798	18.6	0.2	26	1	CF337311	ACCSSION:CF337311
C 726	19	0.3	19	1	AZ648335	ACCSSION:AZ648335	799	18.6	0.2	26	1	AZ437459	ACCSSION:AZ437459
C 727	19	0.3	19	1	AZ649888	ACCSSION:AZ649888	800	18.6	0.2	26	1	AZ771474	ACCSSION:AZ771474
C 728	19	0.3	19	1	AZ764497	ACCSSION:AZ764497	801	18.6	0.2	26	1	BZ593276	ACCSSION:BZ593276
C 729	19	0.3	19	1	AZ764522	ACCSSION:AZ764522	C 802	18.6	0.2	27	1	CF318113	ACCSSION:CF318113
C 730	19	0.3	19	1	AZ764534	ACCSSION:AZ764534	803	18.6	0.2	27	1	AZ495352	ACCSSION:AZ495352
C 731	19	0.3	19	1	AZ770387	ACCSSION:AZ770387	804	18.6	0.2	28	1	AW335064	ACCSSION:AW335064
C 732	19	0.3	19	1	AZ778858	ACCSSION:AZ778858	805	18.6	0.2	28	1	BM549093	ACCSSION:BM549093
C 733	19	0.3	19	1	AZ779901	ACCSSION:AZ779901	806	18.6	0.2	28	1	BM549709	ACCSSION:BM549709
C 734	19	0.3	19	1	AZ781876	ACCSSION:AZ781876	807	18.6	0.2	28	1	BM551130	ACCSSION:BM551130
C 735	19	0.3	19	1	AZ787634	ACCSSION:AZ787634	808	18.6	0.2	28	1	BM551489	ACCSSION:BM551489
C 736	19	0.3	19	1	AZ788058	ACCSSION:AZ788058	809	18.6	0.2	28	1	BM551507	ACCSSION:BM551507
C 737	19	0.3	19	1	AZ789590	ACCSSION:AZ789590	810	18.6	0.2	28	1	BM551765	ACCSSION:BM551765
C 738	19	0.3	19	1	AZ792713	ACCSSION:AZ792713	811	18.6	0.2	28	1	BM551818	ACCSSION:BM551818
C 739	19	0.3	19	1	AZ795403	ACCSSION:AZ795403	812	18.6	0.2	28	1	BM552134	ACCSSION:BM552134
C 740	19	0.3	19	1	AZ801970	ACCSSION:AZ801970	813	18.6	0.2	28	1	BM553072	ACCSSION:BM553072
C 741	19	0.3	19	1	AZ822225	ACCSSION:AZ822225	814	18.6	0.2	28	1	BM553346	ACCSSION:BM553346
C 742	19	0.3	19	1	AZ841581	ACCSSION:AZ841581	815	18.6	0.2	28	1	BM553393	ACCSSION:BM553393
C 743	19	0.3	19	1	AZ841622	ACCSSION:AZ841622	816	18.6	0.2	28	1	BM553451	ACCSSION:BM553451
C 744	19	0.3	19	1	AZ861896	ACCSSION:AZ861896	817	18.6	0.2	28	1	BM553531	ACCSSION:BM553531
C 745	19	0.3	19	1	AZ936798	ACCSSION:AZ936798	818	18.6	0.2	28	1	BM553626	ACCSSION:BM553626
C 746	19	0.3	19	1	AZ985501	ACCSSION:AZ985501	819	18.6	0.2	28	1	BM553647	ACCSSION:BM553647
C 747	19	0.3	19	1	BH000498	ACCSSION:BH000498	820	18.6	0.2	28	1	BM554302	ACCSSION:BM554302
C 748	19	0.3	20	1	AL587572	ACCSSION:AL587572	821	18.6	0.2	28	1	BM554631	ACCSSION:BM554631
C 749	19	0.3	20	1	AL587727	ACCSSION:AL587727	822	18.6	0.2	28	1	BM555415	ACCSSION:BM555415
C 750	19	0.3	20	1	CF282002	ACCSSION:CF282002	823	18.6	0.2	28	1	BM555424	ACCSSION:BM555424
C 751	19	0.3	20	1	CF316662	ACCSSION:CF316662	824	18.6	0.2	28	1	BM555683	ACCSSION:BM555683
C 752	19	0.3	20	1	CF318278	ACCSSION:CF318278	825	18.6	0.2	28	1	BM555705	ACCSSION:BM555705
C 753	19	0.3	20	1	CF320843	ACCSSION:CF320843	826	18.6	0.2	28	1	BM555861	ACCSSION:BM555861
C 754	19	0.3	20	1	AZ341237	ACCSSION:AZ341237	827	18.6	0.2	28	1	BM556242	ACCSSION:BM556242
C 755	19	0.3	20	1	AZ486784	ACCSSION:AZ486784	828	18.6	0.2	28	1	BM556265	ACCSSION:BM556265
C 756	19	0.3	20	1	AZ638704	ACCSSION:AZ638704	829	18.6	0.2	28	1	BM556442	ACCSSION:BM556442
C 757	19	0.3	20	1	AZ821905	ACCSSION:AZ821905	830	18.6	0.2	28	1	BM556491	ACCSSION:BM556491
C 758	19	0.3	20	1	AZ858419	ACCSSION:AZ858419	831	18.6	0.2	28	1	BM556540	ACCSSION:BM556540
C 759	19	0.3	21	1	AL587702	ACCSSION:AL587702	832	18.6	0.2	28	1	BM556549	ACCSSION:BM556549
C 760	19	0.3	21	1	CF302218	ACCSSION:CF302218	833	18.6	0.2	28	1	BM556602	ACCSSION:BM556602
C 761	19	0.3	21	1	CF314260	ACCSSION:CF314260	834	18.6	0.2	28	1	BM557090	ACCSSION:BM557090
C 762	19	0.3	22	1	CF310486	ACCSSION:CF310486	835	18.6	0.2	28	1	BM557380	ACCSSION:BM557380
C 763	19	0.3	22	1	AZ309907	ACCSSION:AZ309907	836	18.6	0.2	28	1	BM557739	ACCSSION:BM557739

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983	17.6	0.2	27	1	BX560901	ACCSSION:BX560901	c1056	17	0.2	21	1	AZ764492	ACCSSION:AZ764492
984	17.6	0.2	27	1	BX562177	ACCSSION:BX562177	1057	17	0.2	22	1	CF310806	ACCSSION:CF310806
985	17.6	0.2	27	1	BX564083	ACCSSION:BX564083	1058	17	0.2	22	1	CF310057	ACCSSION:CF310057
986	17.6	0.2	27	1	CF328811	ACCSSION:CF328811	1059	17	0.2	23	1	BX550903	ACCSSION:BX550903
987	17.6	0.2	27	1	AZ953355	ACCSSION:AZ953355	c1060	17	0.2	24	1	AZ448207	ACCSSION:AZ448207
988	17.6	0.2	27	1	TA165H05P	ACCSSION:TA165H05P	c1061	17	0.2	25	1	AZ468810	ACCSSION:AZ468810
989	17.4	0.2	19	1	AW248747	ACCSSION:AW248747	1062	17	0.2	25	1	AW245275	ACCSSION:AW245275
990	17.4	0.2	19	1	CF291899	ACCSSION:CF291899	1063	17	0.2	25	1	B1094828	ACCSSION:B1094828
991	17.4	0.2	19	1	CF292072	ACCSSION:CF292072	1064	17	0.2	25	1	CF300714	ACCSSION:CF300714
992	17.4	0.2	19	1	CF292144	ACCSSION:CF292144	1065	17	0.2	25	1	CF315032	ACCSSION:CF315032
c 993	17.4	0.2	19	1	CF310688	ACCSSION:CF310688	c1066	17	0.2	25	1	AZ659095	ACCSSION:AZ659095
994	17.4	0.2	19	1	CF329136	ACCSSION:CF329136	c1067	17	0.2	25	1	TA12F02Q	ACCSSION:TA12F02Q
995	17.4	0.2	19	1	AZ633907	ACCSSION:AZ633907	c1068	17	0.2	26	1	AZ658818	ACCSSION:AZ658818
c 996	17.4	0.2	19	1	AZ450180	ACCSSION:AZ450180	c1069	17	0.2	26	1	AZ684666	ACCSSION:AZ684666
997	17.4	0.2	19	1	AZ513919	ACCSSION:AZ513919	c1070	17	0.2	26	1	AZ828616	ACCSSION:AZ828616
998	17.4	0.2	19	1	AZ645841	ACCSSION:AZ645841	c1071	17	0.2	28	1	AA852828	ACCSSION:AA852828
c 999	17.4	0.2	19	1	AZ650252	ACCSSION:AZ650252	1072	17	0.2	30	1	DR31A15T	ACCSSION:DR31A15T
1000	17.4	0.2	19	1	AZ654747	ACCSSION:AZ654747	c1073	17	0.2	31	1	AW245279	ACCSSION:AW245279
1001	17.4	0.2	20	1	CF297010	ACCSSION:CF297010	1074	17	0.2	34	1	BX531309	ACCSSION:BX531309
1002	17.4	0.2	20	1	CF333052	ACCSSION:CF333052	c1075	17	0.2	37	1	BX567522	ACCSSION:BX567522
1003	17.4	0.2	22	1	AZ307896	ACCSSION:AZ307896	1076	16.8	0.2	20	1	CF300961	ACCSSION:CF300961
1004	17.4	0.2	22	1	AZ845735	ACCSSION:AZ845735	1077	16.8	0.2	20	1	CF301101	ACCSSION:CF301101
1005	17.4	0.2	23	1	AZ435597	ACCSSION:AZ435597	1078	16.8	0.2	20	1	CF336815	ACCSSION:CF336815
1006	17.4	0.2	23	1	AZ862224	ACCSSION:AZ862224	c1079	16.8	0.2	20	1	AZ343730	ACCSSION:AZ343730
1007	17.4	0.2	24	1	AZ399663	ACCSSION:AZ399663	c1080	16.8	0.2	20	1	AZ346143	ACCSSION:AZ346143
1008	17.4	0.2	25	1	CF319499	ACCSSION:CF319499	c1081	16.8	0.2	20	1	AZ633741	ACCSSION:AZ633741
1009	17.4	0.2	26	1	AZ65518	ACCSSION:AZ65518	1082	16.8	0.2	21	1	AW248782	ACCSSION:AW248782
1010	17.4	0.2	26	1	AZ818035	ACCSSION:AZ818035	1083	16.8	0.2	21	1	CF319122	ACCSSION:CF319122
1011	17.4	0.2	28	1	AZ844574	ACCSSION:AZ844574	c1084	16.8	0.2	21	1	CF319625	ACCSSION:CF319625
1012	17.4	0.2	28	1	AZ836072	ACCSSION:AZ836072	1085	16.8	0.2	21	1	AZ468862	ACCSSION:AZ468862
1013	17.4	0.2	29	1	CF328476	ACCSSION:CF328476							

c1129	16.8	0.2	30	1	CF2999555	ACCESSION:CF2999555	1202	16.4	0.2	22	1	A2854229	ACCESSION:A2854229
c1130	16.8	0.2	30	1	CF312417	ACCESSION:CF312417	1203	16.4	0.2	23	1	AL587602	ACCESSION:AL587602
c1131	16.8	0.2	30	1	CF322226	ACCESSION:CF322226	1204	16.4	0.2	24	1	CF292725	ACCESSION:CF292725
c1132	16.8	0.2	30	1	CF327835	ACCESSION:CF327835	c1205	16.4	0.2	25	1	A1000095	ACCESSION:A1000095
c1133	16.8	0.2	30	1	CF336555	ACCESSION:CF336555	c1206	16.4	0.2	25	1	A2764498	ACCESSION:A2764498
c1134	16.8	0.2	30	1	A2357603	ACCESSION:A2357603	1207	16.4	0.2	26	1	AZ764502	ACCESSION:AZ764502
c1135	16.8	0.2	30	1	A2443322	ACCESSION:A2443322	1208	16.4	0.2	26	1	A2818035	ACCESSION:A2818035
c1136	16.8	0.2	30	1	A2455741	ACCESSION:A2455741	c1209	16.4	0.2	27	1	N89936	ACCESSION:N89936
c1137	16.8	0.2	30	1	A2481739	ACCESSION:A2481739	1210	16.4	0.2	27	1	TA257807P	ACCESSION:TA257807P
c1138	16.8	0.2	30	1	A2582114	ACCESSION:A2582114	1211	16.4	0.2	27	1	A2812708	ACCESSION:A2812708
c1139	16.8	0.2	31	1	AW249485	ACCESSION:AW249485	1212	16.4	0.2	28	1	A2358038	ACCESSION:A2358038
c1140	16.8	0.2	31	1	EX569502	ACCESSION:EX569502	c1213	16.4	0.2	32	1	RI6114	ACCESSION:RI6114
c1141	16.8	0.2	31	1	CF278807	ACCESSION:CF278807	c1214	16.2	0.2	21	1	A2316019	ACCESSION:A2316019
c1142	16.8	0.2	31	1	CF300345	ACCESSION:CF300345	1215	16.2	0.2	21	1	A2345540	ACCESSION:A2345540
c1143	16.8	0.2	31	1	A2333315	ACCESSION:A2333315	1216	16.2	0.2	21	1	A2346717	ACCESSION:A2346717
c1144	16.8	0.2	31	1	A2375973	ACCESSION:A2375973	1217	16.2	0.2	21	1	A2849030	ACCESSION:A2849030
c1145	16.8	0.2	31	1	A2510092	ACCESSION:A2510092	1218	16.2	0.2	21	1	A2978432	ACCESSION:A2978432
c1146	16.8	0.2	31	1	A2623338	ACCESSION:A2623338	1219	16.2	0.2	22	1	CF318882	ACCESSION:CF318882
c1147	16.8	0.2	31	1	A2627692	ACCESSION:A2627692	1220	16.2	0.2	24	1	CF328535	ACCESSION:CF328535
c1148	16.8	0.2	31	1	A2778697	ACCESSION:A2778697	c1221	16.2	0.2	29	1	BQ590537	ACCESSION:BQ590537
c1149	16.8	0.2	31	1	A2821215	ACCESSION:A2821215	1222	16.2	0.2	32	1	CA853459	ACCESSION:CA853459
c1150	16.8	0.2	31	1	A2826618	ACCESSION:A2826618	c1223	16.2	0.2	32	1	CA853459	ACCESSION:CA853459
c1151	16.8	0.2	31	1	A286763	ACCESSION:A286763	c1224	16.2	0.2	33	1	A2758642	ACCESSION:A2758642
c1152	16.8	0.2	32	1	AW327277	ACCESSION:AW327277	c1225	16.2	0.2	33	1	EX558128	ACCESSION:EX558128
c1153	16.8	0.2	32	1	CF291773	ACCESSION:CF291773	1226	16	0.2	16	1	BQ590166	ACCESSION:BQ590166
c1154	16.8	0.2	32	1	CF299386	ACCESSION:CF299386	1227	16	0.2	16	1	BQ590207	ACCESSION:BQ590207
c1155	16.8	0.2	32	1	CF309233	ACCESSION:CF309233	c1228	16	0.2	16	1	BQ592600	ACCESSION:BQ592600
c1156	16.8	0.2	32	1	CF309345	ACCESSION:CF309345	1229	16	0.2	16	1	BQ592965	ACCESSION:BQ592965
c1157	16.8	0.2	32	1	CF313717	ACCESSION:CF313717	c1230	16	0.2	16	1	BQ595717	ACCESSION:BQ595717
c1158	16.8	0.2	32	1	CF321046	ACCESSION:CF321046	1231	16	0.2	16	1	CF279325	ACCESSION:CF279325
c1159	16.8	0.2	32	1	CF328471	ACCESSION:CF328471	1232	16	0.2	16	1	CF311057	ACCESSION:CF311057
c1160	16.8	0.2	32	1	CF331270	ACCESSION:CF331270	1233	16	0.2	16	1	CF314377	ACCESSION:CF314377
c1161	16.8	0.2	32	1	A2459536	ACCESSION:A2459536	1234	16	0.2	16	1	CF315789	ACCESSION:CF315789
c1162	16.8	0.2	32	1	A2470832	ACCESSION:A2470832	1235	16	0.2	16	1	CF316056	ACCESSION:CF316056
c1163	16.8	0.2	32	1	A2611890	ACCESSION:A2611890	1236	16	0.2	16	1	CF317718	ACCESSION:CF317718
c1164	16.8	0.2	32	1	DR778018	ACCESSION:DR778018	1237	16	0.2	16	1	CF318894	ACCESSION:CF318894
c1165	16.8	0.2	32	1	DR851217	ACCESSION:DR851217	1238	16	0.2	16	1	CF320356	ACCESSION:CF320356
c1166	16.8	0.2	33	1	CF334899	ACCESSION:CF334899	1239	16	0.2	16	1	CF327722	ACCESSION:CF327722
c1167	16.8	0.2	33	1	BU431798	ACCESSION:BU431798	1240	16	0.2	16	1	CF327923	ACCESSION:CF327923
c1168	16.8	0.2	33	1	CF291613	ACCESSION:CF291613	1241	16	0.2	16	1	CF328223	ACCESSION:CF328223
c1169	16.8	0.2	33	1	CF311229	ACCESSION:CF311229	c1242	16	0.2	16	1	CF333386	ACCESSION:CF333386
c1170	16.8	0.2	33	1	CF328967	ACCESSION:CF328967	1243	16	0.2	17	1	BQ590128	ACCESSION:BQ590128
c1171	16.8	0.2	33	1	CF328313	ACCESSION:CF328313	1244	16	0.2	17	1	CF294668	ACCESSION:CF294668
c1172	16.8	0.2	33	1	CF336752	ACCESSION:CF336752	1245	16	0.2	17	1	CF295988	ACCESSION:CF295988
c1173	16.8	0.2	33	1	CF337105	ACCESSION:CF337105	1246	16	0.2	17	1	CF297251	ACCESSION:CF297251
c1174	16.8	0.2	33	1	A2486795	ACCESSION:A2486795	1247	16	0.2	17	1	CF298341	ACCESSION:CF298341
c1175	16.8	0.2	33	1	A2627839	ACCESSION:A2627839	1248	16	0.2	17	1	CF302447	ACCESSION:CF302447
c1176	16.8	0.2	34	1	DR41144T	ACCESSION:DR41144T	1249	16	0.2	17	1	CF313013	ACCESSION:CF313013
c1177	16.6	0.2	23	1	AU267170	ACCESSION:AU267170	1250	16	0.2	17	1	CF336950	ACCESSION:CF336950
c1178	16.6	0.2	23	1	CF300172	ACCESSION:CF300172	1251	16	0.2	19	1	CF300236	ACCESSION:CF300236
c1179	16.6	0.2	23	1	CF302134	ACCESSION:CF302134	1252	16	0.2	19	1	CF309636	ACCESSION:CF309636
c1180	16.6	0.2	23	1	A2374746	ACCESSION:A2374746	c1253	16	0.2	19	1	CF311668	ACCESSION:CF311668
c1181	16.6	0.2	23	1	A2469557	ACCESSION:A2469557	1254	16	0.2	19	1	CF319596	ACCESSION:CF319596
c1182	16.6	0.2	25	1	AV740046	ACCESSION:AV740046	1255	16	0.2	19	1	CF325356	ACCESSION:CF325356
c1183	16.6	0.2	25	1	BG925523	ACCESSION:BG925523	1256	16	0.2	20	1	CF299570	ACCESSION:CF299570
c1184	16.6	0.2	25	1	CF297950	ACCESSION:CF297950	1257	16	0.2	20	1	CF330490	ACCESSION:CF330490
c1185	16.6	0.2	25	1	A2340193	ACCESSION:A2340193	c1258	16	0.2	21	1	CF282313	ACCESSION:CF282313
c1186	16.6	0.2	25	1	A2510562	ACCESSION:A2510562	c1259	16	0.2	21	1	AZ341108	ACCESSION:AZ341108
c1187	16.6	0.2	30	1	AL048684	ACCESSION:AL048684	1260	16	0.2	21	1	A2963501	ACCESSION:A2963501
c1188	16.6	0.2	30	1	AL048732	ACCESSION:AL048732	1261	16	0.2	22	1	AZ317017	ACCESSION:AZ317017
c1189	16.6	0.2	32	1	RS9306	ACCESSION:RS9306	1262	16	0.2	23	1	AW335179	ACCESSION:AW335179
c1190	16.6	0.2	34	1	BM658677	ACCESSION:BM658677	1263	16	0.2	23	1	AZ330773	ACCESSION:AZ330773
c1191	16.4	0.2	18	1	CF304456	ACCESSION:CF304456	c1264	16	0.2	24	1	AU257474	ACCESSION:AU257474
c1192	16.4	0.2	18	1	CF302409	ACCESSION:CF302409	1265	16	0.2	24	1	CF327904	ACCESSION:CF327904
c1193	16.4	0.2	18	1	CF320046	ACCESSION:CF320046	1266	16	0.2	24	1	AZ308225	ACCESSION:AZ308225
c1194	16.4	0.2	19	1	CF329137	ACCESSION:CF329137	1267	16	0.2	24	1	AZ349008	ACCESSION:AZ349008
c1195	16.4	0.2	19	1	CF334610	ACCESSION:CF334610	1268	16	0.2	24	1	AZ805931	ACCESSION:AZ805931
c1196	16.4	0.2	19	1	A2360314	ACCESSION:A2360314	1269	16	0.2	24	1	TA155F12Q	ACCESSION:TA155F12Q
c1197	16.4	0.2	19	1	A2764517	ACCESSION:A2764517	c1270	16	0.2	25	1	CF326989	ACCESSION:CF326989
c1198	16.4	0.2	21	1	CF293087	ACCESSION:CF293087	c1271	16	0.2	26	1	TA321G11P	ACCESSION:TA321G11P
c1199	16.4	0.2	21	1	CF309614	ACCESSION:CF309614	1272	16	0.2	26	1	AU265518	ACCESSION:AU265518
c1200	16.4	0.2	22	1	AZ316361	ACCESSION:AZ316361	c1273	16	0.2	27	1	RS9382	ACCESSION:RS9382

c1275	16	0.2	32	1	CF332296	ACCSSION:CF332296	c1348	15.6	0.2	37	1	BX553095	ACCSSION:BX553095
c1276	15.8	0.2	19	1	CF298134	ACCSSION:CF298134	1349	15.4	0.2	17	1	AW248574	ACCSSION:AW248574
1277	15.8	0.2	19	1	CF298472	ACCSSION:CF298472	1350	15.4	0.2	17	1	BQ591181	ACCSSION:BQ591181
1278	15.8	0.2	19	1	AZ345499	ACCSSION:AZ345499	1351	15.4	0.2	17	1	BQ591588	ACCSSION:BQ591588
1279	15.8	0.2	19	1	AZ509929	ACCSSION:AZ509929	c1352	15.4	0.2	17	1	CF276637	ACCSSION:CF276637
1280	15.8	0.2	19	1	AZ611602	ACCSSION:AZ611602	1353	15.4	0.2	17	1	CF291802	ACCSSION:CF291802
c1281	15.8	0.2	19	1	AZ775624	ACCSSION:AZ775624	1354	15.4	0.2	17	1	CF299997	ACCSSION:CF299997
1282	15.8	0.2	19	1	AZ786336	ACCSSION:AZ786336	1355	15.4	0.2	17	1	CF319075	ACCSSION:CF319075
1283	15.8	0.2	20	1	AW333777	ACCSSION:AW333777	1356	15.4	0.2	18	1	CF329285	ACCSSION:CF329285
c1284	15.8	0.2	20	1	CF331733	ACCSSION:CF331733	c1357	15.4	0.2	19	1	CF326845	ACCSSION:CF326845
c1285	15.8	0.2	20	1	AZ345710	ACCSSION:AZ345710	1358	15.4	0.2	19	1	AZ447251	ACCSSION:AZ447251
1286	15.8	0.2	21	1	CF3313243	ACCSSION:CF3313243	c1359	15.4	0.2	20	1	AZ316368	ACCSSION:AZ316368
c1287	15.8	0.2	21	1	AZ818565	ACCSSION:AZ818565	c1360	15.4	0.2	20	1	AZ369092	ACCSSION:AZ369092
c1288	15.8	0.2	22	1	CF318882	ACCSSION:CF318882	c1361	15.4	0.2	21	1	CF330439	ACCSSION:CF330439
c1289	15.8	0.2	23	1	AZ771221	ACCSSION:AZ771221	1362	15.4	0.2	21	1	AZ831993	ACCSSION:AZ831993
1290	15.8	0.2	24	1	AZ314206	ACCSSION:AZ314206	1363	15.4	0.2	21	1	AZ843343	ACCSSION:AZ843343
c1291	15.8	0.2	24	1	AZ345738	ACCSSION:AZ345738	c1364	15.4	0.2	25	1	TA154D03P	ACCSSION:TA154D03P
c1292	15.8	0.2	24	1	AZ658569	ACCSSION:AZ658569	1365	15.4	0.2	25	1	AZ764498	ACCSSION:AZ764498
1293	15.8	0.2	27	1	AW327923	ACCSSION:AW327923	c1366	15.4	0.2	26	1	CF299646	ACCSSION:CF299646
c1294	15.8	0.2	27	1	CF291968	ACCSSION:CF291968	1367	15.4	0.2	26	1	TA236D08P	ACCSSION:TA236D08P
c1295	15.8	0.2	27	1	CF299084	ACCSSION:CF299084	c1368	15.4	0.2	27	1	N29432	ACCSSION:N29432
c1296	15.8	0.2	27	1	CF329725	ACCSSION:CF329725	c1369	15.4	0.2	27	1	N52529	ACCSSION:N52529
c1297	15.8	0.2	27	1	CF330557	ACCSSION:CF330557	c1370	15.4	0.2	28	1	R37697	ACCSSION:R37697
c1298	15.8	0.2	27	1	CF335229	ACCSSION:CF335229	1371	15.4	0.2	28	1	CF299294	ACCSSION:CF299294
c1299	15.8	0.2	27	1	AZ344642	ACCSSION:AZ344642	c1372	15.4	0.2	29	1	BX567540	ACCSSION:BX567540
c1300	15.8	0.2	27	1	AZ401672	ACCSSION:AZ401672	1373	15.4	0.2	31	1	CF297930	ACCSSION:CF297930
c1301	15.8	0.2	27	1	AZ486791	ACCSSION:AZ486791	c1374	15.4	0.2	32	1	BF032851	ACCSSION:BF032851
c1302	15.8	0.2	27	1	AZ511894	ACCSSION:AZ511894	c1375	15.4	0.2	34	1	CF292071	ACCSSION:CF292071
c1303	15.8	0.2	27	1	AZ580921	ACCSSION:AZ580921	c1376	15.4	0.2	35	1	CF310898	ACCSSION:CF310898
c1304	15.8	0.2	27	1	AZ616094	ACCSSION:AZ616094	1377	15.2	0.2	20	1	CF313751	ACCSSION:CF313751
c1305	15.8	0.2	27	1	AZ623186	ACCSSION:AZ623186	c1378	15.2	0.2	20	1	CF313752	ACCSSION:CF313752
c1306	15.8	0.2	27	1	AZ627847	ACCSSION:AZ627847	1379	15.2	0.2	20	1	CF317946	ACCSSION:CF317946
1307	15.8	0.2	27	1	AZ809295	ACCSSION:AZ809295	1380	15.2	0.2	20	1	CF339443	ACCSSION:CF339443
1308	15.8	0.2	27	1	TA355B06P	ACCSSION:TA355B06P	1381	15.2	0.2	20	1	CF340627	ACCSSION:CF340627
c1309	15.8	0.2	27	1	AZ941721	ACCSSION:AZ941721	c1382	15.2	0.2	20	1	AZ345646	ACCSSION:AZ345646
1310	15.8	0.2	27	1	AZ434285	ACCSSION:AZ434285	c1383	15.2	0.2	20	1	AZ417235	ACCSSION:AZ417235
1311	15.8	0.2	27	1	AZ458228	ACCSSION:AZ458228	1384	15.2	0.2	20	1	AZ592714	ACCSSION:AZ592714
1312	15.8	0.2	28	1	AL048439	ACCSSION:AL048439	1385	15.2	0.2	21	1	AZ626475	ACCSSION:AZ626475
c1313	15.8	0.2	28	1	CF322082	ACCSSION:CF322082	c1386	15.2	0.2	21	1	AZ688662	ACCSSION:AZ688662
1314	15.8	0.2	28	1	CF337400	ACCSSION:CF337400	c1387	15.2	0.2	21	1	AZ625662	ACCSSION:AZ625662
c1315	15.8	0.2	28	1	AZ481286	ACCSSION:AZ481286	c1388	15.2	0.2	21	1	AZ36E11Q	ACCSSION:AZ454378
c1316	15.8	0.2	28	1	T56352	ACCSSION:T56352	c1389	15.2	0.2	22	1	AZ854229	ACCSSION:AZ854229
1317	15.8	0.2	29	1	AZ825156	ACCSSION:AZ825156	1390	15.2	0.2	22	1	AZ470212	ACCSSION:AZ470212
c1318	15.8	0.2	29	1	BQ583967	ACCSSION:BQ583967	c1391	15.2	0.2	22	1	AZ875902	ACCSSION:AZ875902
c1319	15.8	0.2	30	1	BX547779	ACCSSION:BX547779	c1392	15.2	0.2	23	1	AL587602	ACCSSION:AL587602
1320	15.8	0.2	32	1	AZ326012	ACCSSION:AZ326012	1393	15.2	0.2	23	1	AZ308643	ACCSSION:AZ308643
c1321	15.8	0.2	38	1	TA264B08P	ACCSSION:TA264B08P	c1394	15.2	0.2	23	1	AZ345908	ACCSSION:AZ345908
c1322	15.8	0.2	42	1	AZ770047	ACCSSION:AZ770047	1395	15.2	0.2	23	1	AZ468097	ACCSSION:AZ468097
1323	15.6	0.2	22	1	TA303G05P	ACCSSION:TA303G05P	c1396	15.2	0.2	23	1	AZ970753	ACCSSION:AZ970753
c1324	15.6	0.2	22	1	AA99803	ACCSSION:AA99803	c1397	15.2	0.2	26	1	AZ437459	ACCSSION:AZ437459
1325	15.6	0.2	22	1	CF300339	ACCSSION:CF300339	c1398	15.2	0.2	28	1	AW332443	ACCSSION:AW332443
c1326	15.6	0.2	22	1	AZ471736	ACCSSION:AZ471736	c1399	15.2	0.2	28	1	TA327D04P	ACCSSION:TA327D04P
c1327	15.6	0.2	22	1	AZ592068	ACCSSION:AZ592068	c1400	15.2	0.2	29	1	CF314795	ACCSSION:CF314795
1328	15.6	0.2	22	1	AZ633751	ACCSSION:AZ633751	1401	15.2	0.2	29	1	BQ586486	ACCSSION:BQ586486
c1329	15.6	0.2	22	1	TA189G04P	ACCSSION:TA189G04P	c1402	15.2	0.2	29	1	CF312595	ACCSSION:CF312595
c1330	15.6	0.2	23	1	AZ486853	ACCSSION:AZ486853	c1403	15.2	0.2	29	1	CF317850P	ACCSSION:CF317850P
c1331	15.6	0.2	23	1	AZ645254	ACCSSION:AZ645254	c1404	15.2	0.2	29	1	CF336137	ACCSSION:CF336137
c1332	15.6	0.2	23	1	AU012506	ACCSSION:AU012506	1405	15.2	0.2	30	1	AZ962183	ACCSSION:AZ962183
c1333	15.6	0.2	23	1	AZ618720	ACCSSION:AZ618720	c1406	15.2	0.2	31	1	AU268044	ACCSSION:AU268044
c1334	15.6	0.2	23	1	AZ793326	ACCSSION:AZ793326	1407	15.2	0.2	32	1	BG501238	ACCSSION:BG501238
c1335	15.6	0.2	23	1	AZ822888	ACCSSION:AZ822888	c1408	15.2	0.2	32	1	AW250841	ACCSSION:AW250841
1336	15.6	0.2	23	1	AZ984045	ACCSSION:AZ984045	c1409	15.2	0.2	32	1	CF279813	ACCSSION:CF279813
c1337	15.6	0.2	24	1	AZ626101	ACCSSION:AZ626101	c1410	15.2	0.2	32	1	BX558102	ACCSSION:BX558102
c1338	15.6	0.2	24	1	CF281313	ACCSSION:CF281313	c1411	15.2	0.2	32	1	BX560723	ACCSSION:BX560723
1339	15.6	0.2	24	1	AW246443	ACCSSION:AW246443	c1412	15.2	0.2	32	1	BX564047	ACCSSION:BX564047
c1340	15.6	0.2	24	1	AW248929	ACCSSION:AW248929	c1413	15.2	0.2	33	1	BX559212	ACCSSION:BX559212
1341	15.6	0.2	24	1	AZ404465	ACCSSION:AZ404465	c1414	15	0.2	15	1	BE230585	ACCSSION:BE230585
1342	15.6	0.2	25	1	AZ404078	ACCSSION:AZ404078	1415	15	0.2	15	1	BQ582543	ACCSSION:BQ582543
c1343	15.6	0.2	25	1	AW249476	ACCSSION:AW249476	1416	15	0.2	15	1	BQ585820	ACCSSION:BQ585820
c1344	15.6	0.2	26	1	AZ635695	ACCSSION:AZ635695	1417	15	0.2	15	1	BQ590410	ACCSSION:BQ590410
c1345	15.6	0.2	27	1	CF298133	ACCSSION:CF298133	1418	15	0.2	15	1	BQ590656	ACCSSION:BQ590656
c1346	15.6	0.2	32	1	AL587570	ACCSSION:AL587570	1419	15	0.2	15	1	BQ591170	ACCSSION:BQ591170
c1347	15.6	0.2	35	1	BX556508	ACCSSION:BX556508	1420	15	0.2	15	1	BQ591178	ACCSSION:BQ591178

1421	15	0.2	15	1	BQ591223	ACCESION: BQ591223	C1494	15	0.2	25	1	AZ832800	ACCESION: AZ832800
1422	15	0.2	15	1	BQ594689	ACCESION: BQ594689	C1495	15	0.2	25	1	AL587648	ACCESION: AL587648
1423	15	0.2	15	1	CF277319	ACCESION: CF277319	C1496	15	0.2	25	1	AZ381039	ACCESION: AZ381039
1424	15	0.2	15	1	CF281923	ACCESION: CF281923	C1497	15	0.2	25	1	AZ386891	ACCESION: AZ386891
1425	15	0.2	15	1	CF290920	ACCESION: CF290920	C1498	15	0.2	25	1	AZ285663	ACCESION: AZ285663
1426	15	0.2	15	1	CF291029	ACCESION: CF291029	C1499	15	0.2	25	1	T49097	ACCESION: T49097
1427	15	0.2	15	1	CF291103	ACCESION: CF291103	C1500	15	0.2	25	1	TAL3F02Q	ACCESION: TAL3F02Q
1428	15	0.2	15	1	CF291177	ACCESION: CF291177	C1501	15	0.2	26	1	AL587774	ACCESION: AL587774
1429	15	0.2	15	1	CF291798	ACCESION: CF291798	C1502	15	0.2	26	1	AL587774	ACCESION: AL587774
1430	15	0.2	15	1	CF292458	ACCESION: CF292458	C1503	15	0.2	27	1	AZ862643	ACCESION: AZ862643
1431	15	0.2	15	1	CF292461	ACCESION: CF292461	C1504	15	0.2	27	1	R31539	ACCESION: R31539
1432	15	0.2	15	1	CF296652	ACCESION: CF296652	C1505	15	0.2	27	1	CF333518	ACCESION: CF333518
1433	15	0.2	15	1	CF296148	ACCESION: CF296148	C1506	15	0.2	27	1	CF311022	ACCESION: CF311022
1434	15	0.2	15	1	CF298630	ACCESION: CF298630	C1507	15	0.2	27	1	AZ495352	ACCESION: AZ495352
1435	15	0.2	15	1	CF298733	ACCESION: CF298733	C1508	15	0.2	27	1	AZ953355	ACCESION: AZ953355
1436	15	0.2	15	1	CF298805	ACCESION: CF298805	C1509	15	0.2	28	1	AL587605	ACCESION: AL587605
1437	15	0.2	15	1	CF298889	ACCESION: CF298889	C1510	15	0.2	29	1	T67079	ACCESION: T67079
1438	15	0.2	15	1	CF299602	ACCESION: CF299602	C1511	15	0.2	29	1	AL048741	ACCESION: AL048741
1439	15	0.2	15	1	CF299608	ACCESION: CF299608	C1512	15	0.2	29	1	AU267990	ACCESION: AU267990
1440	15	0.2	15	1	CF300121	ACCESION: CF300121	C1513	15	0.2	31	1	TA244G08P	ACCESION: TA244G08P
1441	15	0.2	15	1	CF300361	ACCESION: CF300361	C1514	15	0.2	32	1	AL588429	ACCESION: AL588429
1442	15	0.2	15	1	CF300992	ACCESION: CF300992	C1515	15	0.2	32	1	AZ869514	ACCESION: AZ869514
1443	15	0.2	15	1	CF302034	ACCESION: CF302034	C1516	15	0.2	32	1	BX555533	ACCESION: BX555533
1444	15	0.2	15	1	CF302124	ACCESION: CF302124	C1517	15	0.2	33	1	BX564081	ACCESION: BX564081
1445	15	0.2	15	1	CF302182	ACCESION: CF302182	C1518	14.8	0.2	18	1	AW246505	ACCESION: AW246505
1446	15	0.2	15	1	CF307923	ACCESION: CF307923	C1519	14.8	0.2	18	1	CF329020	ACCESION: CF329020
1447	15	0.2	15	1	CF311159	ACCESION: CF311159	C1520	14.8	0.2	19	1	AI371092	ACCESION: AI371092
1448	15	0.2	15	1	CF311907	ACCESION: CF311907	C1521	14.8	0.2	19	1	CF337608	ACCESION: CF337608
1449	15	0.2	15	1	CF313319	ACCESION: CF313319	C1522	14.8	0.2	19	1	AZ789309	ACCESION: AZ789309
1450	15	0.2	15	1	CF313320	ACCESION: CF313320	C1523	14.8	0.2	20	1	AU007655	ACCESION: AU007655
1451	15	0.2	15	1	CF316251	ACCESION: CF316251	C						

c1567	14.8	0.2	29	1	CF295451	1640	14.2	0.2	19	1	AW249918	ACCESSION:AW249918
c1568	14.8	0.2	29	1	CF299155	1641	14.2	0.2	19	1	AZ331628	ACCESSION:AZ331628
c1569	14.8	0.2	29	1	CF300706	C1642	14.2	0.2	19	1	AZ357587	ACCESSION:AZ357587
c1570	14.8	0.2	29	1	CF295370	C1643	14.2	0.2	19	1	AZ424216	ACCESSION:AZ424216
c1571	14.8	0.2	29	1	CF293772	C1644	14.2	0.2	19	1	AZ447248	ACCESSION:AZ447248
c1572	14.8	0.2	31	1	CF311684	C1645	14.2	0.2	19	1	AZ962226	ACCESSION:AZ962226
c1573	14.8	0.2	31	1	CF312635	C1646	14.2	0.2	19	1	AZ962769	ACCESSION:AZ962769
c1574	14.8	0.2	33	1	AX551140	C1647	14.2	0.2	20	1	AZ486787	ACCESSION:AZ486787
c1575	14.8	0.2	33	1	AX566898	C1648	14.2	0.2	20	1	CF340627	ACCESSION:CF340627
c1576	14.6	0.2	21	1	CF276638	C1649	14.2	0.2	20	1	AU267884	ACCESSION:AU267884
c1577	14.6	0.2	21	1	AZ597932	C1650	14.2	0.2	20	1	AU267884	ACCESSION:AU267884
c1578	14.6	0.2	21	1	CF280925	C1651	14.2	0.2	20	1	BQ586354	ACCESSION:BQ586354
c1579	14.6	0.2	21	1	CF339966	C1652	14.2	0.2	20	1	C53693	ACCESSION:C53693
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c1581	14.6	0.2	21	1	AZ419284	C1654	14.2	0.2	20	1	AZ827842	ACCESSION:AZ827842
c1582	14.6	0.2	21	1	AZ483617	C1655	14.2	0.2	20	1	AZ835133	ACCESSION:AZ835133
c1583	14.6	0.2	21	1	AZ499846	C1656	14.2	0.2	20	1	AZ835133	ACCESSION:AZ835133
c1584	14.6	0.2	21	1	AZ593408	C1657	14.2	0.2	21	1	AZ317208	ACCESSION:AZ317208
c1585	14.6	0.2	21	1	AZ589098	C1658	14.2	0.2	21	1	AZ853429	ACCESSION:AZ853429
c1586	14.6	0.2	21	1	AZ627978	C1659	14.2	0.2	21	1	AZ346714	ACCESSION:AZ346714
c1587	14.6	0.2	21	1	AZ770188	C1660	14.2	0.2	21	1	AZ399828	ACCESSION:AZ399828
c1588	14.6	0.2	21	1	AZ961893	C1661	14.2	0.2	21	1	AZ475883	ACCESSION:AZ475883
c1589	14.6	0.2	22	1	AZ374487	C1662	14.2	0.2	21	1	AZ654730	ACCESSION:AZ654730
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c1591	14.6	0.2	22	1	AU260373	C1664	14.2	0.2	21	1	AZ809249	ACCESSION:AZ809249
c1592	14.6	0.2	22	1	AZ47246	C1665	14.2	0.2	21	1	AZ936997	ACCESSION:AZ936997
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c1598	14.6	0.2	22	1	AZ778745	C1671	14.2	0.2	28	1	CF277114	ACCESSION:CF277114
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c1601	14.6	0.2	22	1	AZ974046	C1674	14.2	0.2	31	1	AX559254	ACCESSION:AX559254
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c1603	14.6	0.2	23	1	AZ380872	C1676	14.2	0.2	32	1	AX553142	ACCESSION:AX553142
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c1605	14.6	0.2	26	1	AZ485624	C1678	14.2	0.2	35	1	AX861400	ACCESSION:AX861400
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c1607	14.6	0.2	27	1	T52979	C1680	14	0.2	14	1	BQ587890	ACCESSION:BQ587890
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c1617	14.4	0.2	20	1	AZ368518	C1690	14	0.2	14	1	CF277935	ACCESSION:CF277935
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c1619	14.4	0.2	22	1	AZ764528	C1692	14	0.2	14	1	CF278452	ACCESSION:CF278452
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c1621	14.4	0.2	24	1	AZ764519	C1694	14	0.2	14	1	CF279992	ACCESSION:CF279992
c1622	14.4	0.2	24	1	TA155F12Q	C1695	14	0.2	14	1	CF281958	ACCESSION:CF281958
c1623	14.4	0.2	24	1	AW248929	C1696	14	0.2	14	1	CF282350	ACCESSION:CF282350
c1624	14.4	0.2	25	1	CF638767	C1697	14	0.2	14	1	CF294449	ACCESSION:CF294449
c1625	14.4	0.2	25	1	N33150	C1698	14	0.2	14	1	CF295570	ACCESSION:CF295570
c1626	14.4	0.2	25	1	CF317007	C1699	14	0.2	14	1	CF296120	ACCESSION:CF296120
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c1628	14.4	0.2	25	1	AZ867155	C1701	14	0.2	14	1	CF298109	ACCESSION:CF298109
c1629	14.4	0.2	25	1	AZ348233	C1702	14	0.2	14	1	CF299368	ACCESSION:CF299368
c1630	14.4	0.2	26	1	CF296851	C1703	14	0.2	14	1	CF300542	ACCESSION:CF300542
c1631	14.4	0.2	26	1	R26779	C1704	14	0.2	14	1	CF301020	ACCESSION:CF301020
c1632	14.4	0.2	27	1	AZ382581	C1705	14	0.2	14	1	CF301083	ACCESSION:CF301083
c1633	14.4	0.2	29	1	TA239G06Q	C1706	14	0.2	14	1	CF301380	ACCESSION:CF301380
c1634	14.4	0.2	29	1	AX557758	C1707	14	0.2	14	1	CF302675	ACCESSION:CF302675
c1635	14.4	0.2	29	1	AX561329	C1708	14	0.2	14	1	CF302846	ACCESSION:CF302846
c1636	14.4	0.2	33	1	AL048719	C1709	14	0.2	14	1	CF308006	ACCESSION:CF308006
c1637	14.4	0.2	34	1	AL047464	C1710	14	0.2	14	1	CF308220	ACCESSION:CF308220
c1638	14.2	0.2	19	1	AZ513919	C1711	14	0.2	14	1	CF308445	ACCESSION:CF308445
c1639	14.2	0.2	19	1	AZ645841	C1712	14	0.2	14	1	CF308918	ACCESSION:CF308918

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0289 row: I column: 06
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 50.

FEATURES

source

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 /organism="Mus musculus"
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 /db_xref="taxon:10090"
 /clone="UUGC1M0289106"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 34.8; DB 1; Length 50;
 Best Local Similarity 94.7%; Pred. No. 3.7;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1923 TGGCATTAAACATCTCTAGTCCACACCGCGCTCG 1960
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 Db 50 TGGCATTAAACATCTCTAGTCCACACCGCGGTATG 13

RESULT 3

AZ861400
 LOCUS 2M0167013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC2M0167013 R, genomic survey sequence.

ACCESSION AZ861400

VERSION AZ861400.1 GI:13057682

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 35)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0167 row: O column: 13
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 35.

FEATURES

Location/Qualifiers

source

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 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="UUGC2M0167013"
 /sex="Male"
 /lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 27.8; DB 1; Length 35;
 Best Local Similarity 93.5%; Pred. No. 28;
 Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 |||||
 Db 1 AGCAGCAGCAGCAGCAGCAGCAGCAGCA 31

RESULT 4

AZ987023

LOCUS

DEFINITION 2M0269N24F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0269N24 F, genomic survey sequence.

ACCESSION AZ987023

VERSION AZ987023.1 GI:13858250

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 39)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

REFERENCE

AUTHORS

1 (bases 1 to 39)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

```

Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: N column: 24
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 39.
Location/Qualifiers
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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GII4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.3%; Score 25.4; DB 1; Length 39;
Best Local Similarity 82.9%; Pred. No. 1e+02;
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 5314 TGTTCTCTCTTTTCTCTCTTTGGCTTCATCTCTC 5348
Db 1 TGTTCTCTCTTTTCTCTCTTTCTCTCTCTCTC 35

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Query Match	0.3%; Score 25.4; DB 1; Length 39;
Best Local Similarity	82.9%; Pred. No. 1e+02;
Matches	29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY	5314 TGTTCTCTCTTTCTCTCTTTGGCTTCACATCTCTC 5348
DB	1
	1 TGTTCTCTCTTTCTCTCTTTGGCTTCACATCTCTCTC 35
RESULT 5	
TA264B08P	
LOCUS	TA264B08P 38 bp DNA linear GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 264B08, forward sequence, genomic survey sequence.
ACCESSION	AL483993
VERSION	AL483993.1 GI:11849953
KEYWORDS	GSS.
SOURCE	Trypanosoma brucei
ORGANISM	Trypanosoma brucei
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE	1 (bases 1 to 38)
AUTHORS	Hall N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ()
	4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

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FEATURES
source
1..38
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/db_xref="taxon:5691"
/clone="264b08"

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Best Local Similarity 78.9%; Pred. No. 1e+02;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 4451 GGGTGGCATGGACCTTTTGTGTCCT 4488
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D6 1 GGGGGGGGGGGTTTTTTTTTTTTTTT 38

RESULT 6
AZ404206/c

LOCUS AZ404206 27 bp DNA linear GSS 03-OCT-2000
DEFINITION IM01721220F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M01721220 F, genomic survey sequence.
ACCESSION AZ404206
VERSION AZ404206.1 GI:10528219
KEYWORDS GSS.

REMARKS	SOURCE
	Mus musculus (house mouse)

ORGANISM	Mus musculus
REFERENCE	1 (bases 1 to 27)
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

CONTACT Unpublished (2000)

COMMENT Contact: Robert B. Weiss

CONTACT: ROBERT D. HARRIS
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Phone: 801.303.7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0172 row: I column: 20

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends
High quality: commoner stores: 22

High quality sequence stop: 27.
Location/Qualifiers

FEATURES	LOCATION/Qualifiers
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source
2. 127
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/seq="Mol..."
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/clone_lib="Mouse 10kb
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/clone_112= mouse 10kb
/note="Vector: PWP42nv"
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musculus C57BL/6J (male)

Laboratory Mouse DNA R

(<http://www.jax.org/re>

was hydrodynamically s

0.005 inch orifice at
was blunt and remained

was blunt end-repaired
polynucleotide kinase

потупистеостиде кинаве:

FEATURES
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers

FEATURES

CF328492	LOCUS	34 bp	mRNA	linear	EST 18-AUG-2003
DEFINITION	NACL--03-G22.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--03-G22, mRNA sequence.				
ACCESSION	CF328492				
VERSION	CF328492.1	GI:33805230			
KEYWORDS	EST.				
SOURCE	Oryza sativa				
ORGANISM	Oryza sativa				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.				
AUTHORS	Kim, D.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, Y.-K., Kim, Y.-K. and Nahm, B.H.				
TITLE	Large-scale Sequencing Analysis of Rice ESTs				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea Tel.: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.				
FEATURES	Location/Qualifiers				
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	/clone="NACL--03-G22"				
	/tissue_type="callus"				
	/dev_stage="proliferated callus on 2N6 media for 30 days"				
	/lab_host="E. coli DH108"				
	/clone_lib="rice callus plasmid cDNA library (NACL)"				
	/notes="vector: PCR-TOP0; Site1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."				
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Best Local Similarity	86.7%;	Pred. No. 1.5e+02;			
Matches	26;	Conservative	0;	Mismatches	4;
				Indels	0;
				Gaps	0;
QY	4467	TTTTTTTTTTTTTTTTTTGCTTGAGACATG	4496		
Db	1	TTTTTTTTTTTTTTTTTTTACACATG	30		
RESULT 16	AZ485624/c				
LOCUS	AZ485624				
DEFINITION	1M0313H1LF Mouse 10kb plasmid UGCLIM library Mus musculus genomic clone UGCLIM0313H1 F, genomic survey sequence.				
ACCESSION	AZ485624				
VERSION	AZ485624.1	GI:10651606			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1' (bases 1 to 26)				
	Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				


```

source
1. .30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261I24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 23.4; DB 1; Length 30;
Best Local Similarity 96.0%; Pred. No. 1.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTT 4488
Db 3 TTTTGTCTT 27

RESULT 20
BX564081 33 bp mRNA linear EST 10-OCT-2003
LOCUS
DEFINITION
BX564081 Glossina morsitans moritans adult infected gut Glossina morsitans moritans cDNA clone Tse6f01_p1c, mRNA sequence.
ACCESSION
BX564081
VERSION
BX564081.1 GI:33431278
KEYWORDS
EST.
SOURCE
Glossina morsitans moritans
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.P., Lehane, S. and Hall, N.
TITLE
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans moritans and expression analysis of putative immune response genes
JOURNAL
Genome Biol. 4 (10), R63 (2003)
MEDLINE
22881942
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.
Location/Qualifiers

source
1. .33
/organism="Glossina morsitans moritans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse6f01_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans moritans adult infected gut"
/notes="Country: Zimbabwe; EST from adult gut infected with T. brucei"

Query Match 0.3%; Score 23.4; DB 1; Length 33;
Best Local Similarity 96.0%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTGTCTT 4486
Db 9 AGTTTGTCTT 33

RESULT 21
CF334899 33 bp mRNA linear EST 18-AUG-2003
LOCUS
DEFINITION
CF334899 JMT--04-F19-g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--04-F19, mRNA sequence.
ACCESSION
CF334899
VERSION
CF334899.1 GI:33818141
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 33)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

source
1. .33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--04-F19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/notes="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 23.4; DB 1; Length 33;
Best Local Similarity 96.0%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTT 4488
Db 5 TTTTGTCTT 29

RESULT 22

```


LOCUS	29 bp	mRNA	linear	EST
T67079				07-MAR-1995
DEFINITION	Soares fetal liver spleen INFLS	Homo sapiens cDNA clone		


```

AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgabs-r@mail.nih.gov
             CDNA Library Preparation: Life Technologies, Inc.
             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM10809  row: e  column: 12
             High quality sequence stop: 30.

FEATURES     source
             1. 30
             /organism="Mus musculus"
             /mol_type="mRNA"
             /strain="FVB/N"
             /db_xref="taxon:10090"
             /clone="IMAGE:4909811"
             /lab_host="DH10B (TI phage-resistant)"
             /clone_lib="NCI CGAP SG2"
             /notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1:
             NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
             dt. Average insert size 1.3 kb. Constructed by Life
             Technologies. Note: this is a NCI CGAP Library."

Query Match      0.3%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 30 CTTTCTTTTCTTTTCTTTTCTTTTCTTT 5

RESULT 34
AZ962183/c
LOCUS        AZ962183
DEFINITION   2M0230124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0230124 R, genomic survey sequence.
ACCESSION    AZ962183
VERSION      AZ962183.1  GI:13833410
KEYWORDS     GSS.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             1 (bases 1 to 30)
REFERENCE    1
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
             Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
             Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
             Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0230 row: I column: 24
             Seq primer: CACACGGAACACCTATGACC
             Class: plasmid ends
             High quality sequence stop: 30.
             Location/Qualifiers
             1. 30
             /organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0230124"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 22.8; DB 1; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.5e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 27 CTTTCTTTTCTTTTCTTTTCTTTTCTTT 2

RESULT 35
BG292912/c
LOCUS        BG292912
DEFINITION   602389549F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:4501164 5',
mRNA sequence.
ACCESSION    BG292912
VERSION      BG292912.1  GI:13052227
KEYWORDS     EST.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
             1 (bases 1 to 31)
REFERENCE    1
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
             Email: cgabs-r@mail.nih.gov
             Tissue Procurement: The Cepko Laboratory
             CDNA Library Preparation: Life Technologies, Inc.
             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM10368  row: b  column: 13
             High quality sequence stop: 31.
             Location/Qualifiers
             1. 31
             /organism="Mus musculus"
             /mol_type="mRNA"
             /db_xref="taxon:10090"
             /clone="IMAGE:4501164"
             /tissue_type="retina"
             /lab_host="DH10B (phage-resistant)"
             /clone_lib="NIH MGC 94"
             /note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;

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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Query Match 0.3%; Score 22.8; DB 1; Length 31;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTTGTCT 4488
Db 31 CTTTTTTTTTTTTTTTTTTT 6

RESULT 36
AL587570 32 bp mRNA linear EST 02-MAR-2001
LOCUS
DEFINITION AL587570 BP Chicken Brain Library Gallus gallus cDNA clone
RO5059B09, mRNA sequence.
ACCESSION AL587570
VERSION AL587570.1 GI:13192604
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 32)
AUTHORS Murray, F.
TITLE BP Chicken Brain Library
JOURNAL Unpublished (2001)
COMMENT Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetechn
(*6854-
Seq primer: M13F.
Location/Qualifiers
1. 32
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059B09"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: oligo dt. 5' adaptor sequence:
5' TCGACCTCGAG 3'; 3' adaptor sequence: 5'
GCGGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
Clonetechn (*6854-1)"

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4465 TTTTTTTTTTTTTTTTTTGTCTGA 4490
Db 3 TTTTTTTTTTTTTTTTTTCTTA 28

RESULT 37
CF302459/c 32 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION 7LEAF--08-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-A01, mRNA sequence.
ACCESSION CF302459
VERSION CF302459.1 GI:33674220

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4465 TTTTTTTTTTTTTTTTTTGTCTGA 4490
Db 3 TTTTTTTTTTTTTTTTTTCTTA 28

RESULT 37
CF302459/c 32 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION 7LEAF--08-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-A01, mRNA sequence.
ACCESSION CF302459
VERSION CF302459.1 GI:33674220

KEYWORDS
SOURCE
ORGANISM

EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 32)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 32)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source

1. 32
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--08-A01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTGTCTTG 4489
Db 28 TTTTTTTTTTTTTTTTTTTTG 3

RESULT 38
AZ579652

LOCUS
DEFINITION AZ579652 32 bp DNA linear GSS 13-DEC-2000
1M0367C12R Mouse 10kb plasmid UGCCIM library Mus musculus genomic
clone UGCCIM0367C12 R, genomic survey sequence.
ACCESSION AZ579652
VERSION AZ579652.1 GI:11694081
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 12
Seq primer: CACACAGGAACAGCTATGACC

REFERENCE
AUTHORS

1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 12
Seq primer: CACACAGGAACAGCTATGACC

TITLE
JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0367 row: C column: 12
Seq primer: CACACAGGAACAGCTATGACC

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Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0367C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTTTGCTT 4488
DB 2 CTTTTTTTTTTTTTTTTTTT 27

RESULT 39
LOCUS DRI1F7S 32 bp DNA linear GSS 27-NOV-2002
DEFINITION Danio rerio genomic clone DKEX-1F7, genomic survey sequence.
ACCESSION AL735323
VERSION AL735323.1 GI:21343938
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 32)
Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 1F7. 1F7 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. .32
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-1F7"
/tissue_type="Testis"
/notes="vector pindigoBAC-536"

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.8; DB 1; Length 33;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTGCTTG 4489
DB 6 TTTTTTTTTTTTTTTTTTTT 31

RESULT 40
LOCUS AZ759642 33 bp DNA linear GSS 16-FEB-2001
DEFINITION clone UUGC1M0552E03 R, genomic survey sequence.
ACCESSION AZ759642
VERSION AZ759642.1 GI:12866639
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: E column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.8; DB 1; Length 33;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTTCTT 4488
Db 3 CTTTTTTTTTTTTTTTTTTT 28

RESULT 41
AV674152
LOCUS
DEFINITION AV674152 Nori Satoh unpublished cDNA library Ciona intestinalis
ACCESSION AV674152
VERSION AV674152.1 GI:10112151
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE 1 (bases 1 to 34)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoheascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..34
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="citb14i22"
/tissue_type="whole animal"
/dev_stages="tailbud"
/clone_lib="Nori Satoh unpublished cDNA library"

Query Match 0.3%; Score 22.8; DB 1; Length 34;
Best Local Similarity 92.3%; Pred. No. 2.1e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTTCTT 4488
Db 2 CTTTTTTTTTTTTTTTTTTT 27

RESULT 42
CF292071
LOCUS
DEFINITION CF292071 14ROOT--02-M02.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-M02, mRNA sequence.
ACCESSION CF292071
VERSION CF292071.1 GI:33661104
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source
1..34
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="7LEAF--07-J10"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 34;
Best Local Similarity 92.3%; Pred. No. 2.1e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTTCTT 4488
Db 2 CTTTTTTTTTTTTTTTTTTT 27

RESULT 42
CF292071
LOCUS
DEFINITION CF292071 14ROOT--02-M02.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-M02, mRNA sequence.
ACCESSION CF292071
VERSION CF292071.1 GI:33661104
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 34)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
source
1..34
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="taxon:4530"
/clone="7LEAF--07-J10"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 34;
Best Local Similarity 92.3%; Pred. No. 2.1e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTTCTT 4488
Db 8 CTTTTTTTTTTTTTTTTTTT 33

```

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source

```

1..34
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-M02"
/tissue_type="root"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.3%; Score 22.8; DB 1; Length 34;

Best Local Similarity 79.4%; Pred. No. 2.1e+02;

Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4469 TTTTTTTTTTTTTTGTCTTGACATGGGGTTT 4502

Db 1 TTTTTTTTTTTTTTGTCTTGACATGGGGTTT 34

RESULT 43

CF302250

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 34)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1..34

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--07-J10"

/tissue_type="leaf"

/dev_stages="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 34;

Best Local Similarity 92.3%; Pred. No. 2.1e+02;

Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTGTCTTCTTG 4489

Db 8 TTTTTTTTTTTTTTGTCTTCTTG 33

```

RESULT 44
TA68D10P
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 68d10, forward sequence,
genomic survey sequence.
ACCESSION AL457502
KEYWORDS AL457502.1 GI:11858728
SOURCE GSS.
ORGANISM Trypanosoma brucei
            Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE 1 (bases 1 to 34)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES
            source
            1..34
                /organism="Trypanosoma brucei"
                /mol_type="genomic DNA"
                /strain="TREU927"
                /db_xref="taxon:5691"
                /clones="68d10"
Query Match 0.3%; Score 22.8; DB 1; Length 34;
Best Local Similarity 79.4%; Pred. No. 2.1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4447 GGGTGGTGGCATGGACTTTTTTTTTTTT 4480
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGGGGGGGGGGGGGGT 34
Query Match 0.3%; Score 22.8; DB 1; Length 34;
Best Local Similarity 79.4%; Pred. No. 2.1e+02;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 4447 GGGTGGTGGCATGGACTTTTTTTTTTTT 4480
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GGGGGGGGGGGGGGGGGT 34
RESULT 45
BF338797/c
LOCUS
DEFINITION 602036229F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184167
5', mRNA sequence.
ACCESSION BF338797
KEYWORDS BF338797.1 GI:11285216
SOURCE EST.
ORGANISM Homo sapiens (human)
            Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 35)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LIAW501 row: j column: 08
High quality sequence stop: 30.

FEATURES

source

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1..35
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4184167"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Brn64"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NCI; Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.57 Kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

```

Query Match 0.3%; Score 22.8; DB 1; Length 35;
Best Local Similarity 92.3%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTTTTTTTTTTTTTGTCTT 4488

Db 33 CTTTCTTTTTTTTTTTTTTTT 8

RESULT 46

AZ819924/c

LOCUS

DEFINITION

2M0091A19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0091A19 R, genomic survey sequence.

AZ819924

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: A column: 19
Seq primer: CACACAGGAACACGATATGACC
Class: plasmid ends
High quality sequence stop: 29.

FEATURES

source

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1..29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.6; DB 1; Length 29;
Best Local Similarity 86.2%; Pred. No. 1.5e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4460 GGACTTTTTTTTTTTTTTTTTTTCTCT 4488
DB 29 GGGTTTTTTTTTTTTTTTTTTTTTTT 1

RESULT 47
R16114
LOCUS
DEFINITION
Yas51f03.s2 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:66461 3' similar to gb:M93426 PROTEIN-TYROSINE PHOSPHATASE
ZETA PRECURSOR (HUMAN); mRNA sequence.

ACCESSION
R16114
VERSION
KEYWORDS
SOURCE
EST.
R16114.1 GI:767923
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)

REFERENCE
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:66461"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)"

FEATURES
source
1. 32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:66461"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen INFLS"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)"

with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGTAATTAAGATCTTTTTTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.3%; Score 22.6; DB 1; Length 32;
Best Local Similarity 78.1%; Pred. No. 1.9e+02;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4465 TTTTTTTTTTTTTTTTTGCTTGAGACATG 4496
DB 1 TTTTTTTTTTTTTTTTTTNTTNTATG 32

RESULT 48
R59306
LOCUS
DEFINITION
Yh16c10.s1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:37903 3' similar to gb:M29064 HETEROGENEOUS NUCLEAR
RIBONUCLEOPROTEINS A2/B1 (HUMAN); mRNA sequence.

ACCESSION
R59306
VERSION
KEYWORDS
SOURCE
EST.
R59306.1 GI:830001
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 32)

REFERENCE
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: SP6
High quality sequence stop: 1.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:37903"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AACTGGAAGTAATTCGCCGCCGAGATTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES
source
1. 32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:410444"
/db_xref="taxon:9606"
/clone="IMAGE:37903"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AACTGGAAGTAATTCGCCGCCGAGATTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.3%; Score 22.6; DB 1; Length 32;
 Best Local Similarity 86.2%; Pred. No. 1.9e+02;
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4464 TTTT...TTTGTCTTGAGA 4492
 |||||
 Db 3 TTTT...TTTCCCTTAGA 31

RESULT 49
 LOCUS AU013658 33 bp mRNA linear EST 03-AUG-1998
 DEFINITION AU013658 Schizosaccharomyces pombe late log phase cDNA
 Schizosaccharomyces pombe cDNA clone spc08464, mRNA sequence.
 AU013658
 ACCESSION AU013658.1 GI:3368449
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Schizosaccharomyces pombe (fission yeast)
 Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS Morimyo M. and Mita K.
 TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe

JOURNAL Unpublished (1998)
 COMMENT Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-Ku, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.
 Location/Qualifiers

FEATURES
 source 1..33
 /organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc08464"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

Query Match 0.3%; Score 22.6; DB 1; Length 33;
 Best Local Similarity 86.2%; Pred. No. 2.1e+02;
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4464 TTTT...TTTGTCTTGAGA 4492
 |||||
 Db 4 TTTT...TTTAAAA 32

RESULT 50
 LOCUS AW334249 34 bp mRNA linear EST 31-JAN-2000
 DEFINITION S2D4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
 ACCESSION AW334249
 VERSION AW334249.1 GI:6830606
 KEYWORDS
 SOURCE
 ORGANISM Pneumocystis carinii
 Pneumocystis carinii
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
 Pneumocystidaceae; Pneumocystis.
 REFERENCE 1 (bases 1 to 34)
 AUTHORS Smullan, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.
 TITLE Expressed sequence tags from Pneumocystis carinii

JOURNAL Unpublished (2000)
 COMMENT Contact: Staben C
 School of Biological Sciences
 University of Kentucky
 101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA
 Tel: 606 257 2161
 Fax: 606 257 1717
 Email: staben@pop.uky.edu.
 Location/Qualifiers

FEATURES
 source 1..34
 /organism="Pneumocystis carinii"
 /mol_type="mRNA"
 /db_xref="taxon:4754"
 /lab_host="E. coli"
 /clone_lib="AGS-1"
 /notes="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat [99-1-6, sacrificed on 3/17/99] at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.3%; Score 22.6; DB 1; Length 34;
 Best Local Similarity 86.2%; Pred. No. 2.2e+02;
 Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4464 TTTT...TTTGTCTTGAGA 4492
 |||||
 Db 5 TTTT...TTTAAAA 33

RESULT 51
 LOCUS AZ345610/c 34 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M080C24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080C24 F, genomic survey sequence.

ACCESSION AZ345610 1 GI:10424847
 VERSION
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 34)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weis, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plates: 0080 row: C column: 24
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 34.
 Location/Qualifiers

FEATURES
 source 1..34
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0080C24"
 /sex="Male"


```

FEATURES
source
high quality sequence stop: 32.
Location/Qualifiers
1. .32
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3959127"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 66"
/notes="Ovary; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "
0.3%; Score 22.4; DB 1; Length 32;
Query Match

```



```

/clone="UUGC1M0162P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4462 ACTTTTGTCTT 4488
Db 30 AATTTTTTTTTTTTTTTTTTTTTT 4

RESULT 59
AZ400441/c
LOCUS
DEFINITION
M10166C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0166C14 R, genomic survey sequence.
ACCESSION
AZ400441
VERSION
AZ400441.1 GI:10515515
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weise,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: C column: 14
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0166C14"

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4462 ACTTTTGTCTT 4488
Db 32 AATTTTTTTTTTTTTTTTTTTTTT 6

RESULT 60
AL587609
LOCUS
DEFINITION
AL587609 BP Chicken Brain Library Gallus gallus cdna clone
ROS059G05, mRNA sequence.
ACCESSION
AL587609.1 GI:13192643
VERSION
EST.
KEYWORDS
Gallus gallus (chicken)
SOURCE
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 33)
Murray,F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCGTGTGTGTGTGTGTGTGT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
1..33
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059G05"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5',
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5',
GCGGCGCGTGTGTGTGTGTGTGTGT 3' Poly A RNA purchased from

```

RESULT	62
AL587876	
LOCUS	
DEFINITION	AL587876 BP Chicken Brain Library Gallus gallus cdna clone
ACCESSION	AL587876
	ROS064F10, mRNA sequence.
	34 bp mRNA linear EST 02-MAR-2001

Email: gyapuzs@email.llnl.gov
 Tissue Procurement: ARCC
 CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM528 row: k column: 07
 High quality sequence stop: 34.


```

REFERENCE
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah
              Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0181 row: 1 column: 07
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 32.
              Location/Qualifiers
FEATURES             source
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0181I07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match          0.3%; Score 22; DB 1; Length 32;
Best Local Similarity 83.3%; Pred. NO. 2.5e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4465 TTTTGTGCTTCGACACA 4494
Db 31 TTTTGTGCTTCGACACA 2

RESULT 67
AL048719/c          AL048719          33 bp      mRNA      linear      EST 04-SEP-2003
LOCUS              DKFZp566G233_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DEFINITION          DKFZp566G233, mRNA sequence.
ACCESSION           AL048719
VERSION             AL048719.1 GI:4727790
KEYWORDS            EST.
SOURCE              Homo sapiens (human)
ORGANISM            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS      Koshner,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
1 (bases 1 to 33)
EST (Koshner, et al.)
JOURNAL
COMMENT      Unpublished (1999)
              Contact: MIPS
              MIPS
              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             source
1..33
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566G233"
/tissue_type="kidney"
/dev stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pMW1; Site_1: NotI; Site_2: SalI"
Query Match          0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. NO. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTGTGCTTCGTTGT 4485
Db 33 TTTTGTGCTTCGTTGT 12

RESULT 68
BX551140            BX551140            33 bp      mRNA      linear      EST 10-OCT-2003
LOCUS              BX551140 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION          morsitans morsitans cDNA clone Teel16g12_pic, mRNA sequence.
ACCESSION           BX551140
VERSION             BX551140.1 GI:33374994
KEYWORDS            EST.
SOURCE              Glossina morsitans morsitans
ORGANISM            Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 33)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL             Genome Biol. 4 (10), R63 (2003)
MEDLINE             22881942
PUBMED              14519198
COMMENT             Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES             source
1..33
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Teel16g12 pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with

```



```

T.brucei"

Query Match      0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTGCTT 4488
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTGTTTT 33

RESULT 69
BX553142
LOCUS BX553142 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse127f01_pic, mRNA sequence.
ACCESSION BX553142
VERSION BX553142.1 GI:33377335
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 33)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1. .33
/mol_type="mRNA"
/organism="Glossina morsitans morsitans"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse127f01_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTGCTT 4488
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTGTTTT 33

RESULT 71
CF291048
LOCUS CF291048 25 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-F05, mRNA sequence.
ACCESSION CF291048
VERSION CF291048.1 GI:33660081
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,F.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

T.brucei"

Query Match      0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTGT 4485
Db 12 TTTTTTTTTTTTTTTTTTTGT 33

RESULT 70
BX566898
LOCUS BX566898 33 bp mRNA linear EST 14-OCT-2003
DEFINITION BX566898 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse84h03_pic, mRNA sequence.
ACCESSION BX566898

```

99 TTTTTTTTTTTTTTTTTTTT

REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

```

1. 26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS-07-L18"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred.No.1.6e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
      |||||
Db 26 TTTTTTTTTTTTTTTTTTTT

RESULT 95
CF299701
LOCUS
DEFINITION
CF299701 26 bp mRNA linear EST 15-AUG-2003
7LEAF--03-N03.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-N03, mRNA sequence.

```

ORGANISM	Oryza sativa
REFERENCE	1 (bases 1 to 26)
AUTHORS	Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.
FEATURES	Location/Qualifiers
source	1..26 /organism="Oryza sativa" /mol_type="mRNA" /cultivar="Nackdong" /db_xref="taxon:4530" /clone="7LEAF-03-N03" /issue_type="leaf" /dev_stage="7 days after germination" /lab_host="E. coli DH10B"

```

/clone_lib=Rice leaf plasmid cDNA library II (7LEAF)"
/notes=Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 21.8; DB 1; Length 26;
Best Local Similarity 92.0%; Pred. No. 1.6e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
      |||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTT 25

RESULT 96
CF302874
LOCUS 7LEAF--08-M19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--08-M19, mRNA sequence.
EST 15-AUG-2003

```

CF5028/4.1 GI:33674635
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza..
1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@cbio.com, bhnahm@bio.myongji.ac.kr.

[illegible]

with adaptors complementary to the insert adaptors and

purified. The she

purified. The she

Query Match	0.3%;	Score 21.8;	DB 1;	Length 26;
Best Local Similarity	92.0%;	Pred. No. 1.6e+02;		

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4464 TTTT...TTTTCCTT 4488
 Db 1 TTTT...TTTTCCTT 25

RESULT 110
 TA324D07P/c 26 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 324D07, forward sequence,
 DEFINITION genomic survey sequence.

ACCESSION AL493390 GI:11867755
 VERSION AL493390.1
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajadream, M.A. and Barrell, B.G.

TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Barrell, Oxford University Press, 1999).

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
 source
 1..26
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="324d07"

Query Match 0.3%; Score 21.8; DB 1; Length 26;
 Best Local Similarity 92.0%; Pred. No. 1.6e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTCCTT 4488
 Db 26 TTTT...TTTTCCTT 2

RESULT 111
 AW327923/c 27 bp mRNA linear EST 28-JAN-2000
 LOCUS dr02g08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA
 DEFINITION sequence.

ACCESSION AW327923
 VERSION AW327923.1 GI:6798418
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 27)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Edge Biosystems
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/image/image.html
 Plate: LLCM0029 row: M column: 16
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..27
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847159"
 /tissue_type="Burkitt lymphoma"
 /cell_line="MGC4"
 /clone_lib="NIH_MGC_3"
 /note="Organ: Lymph; Vector: pOTB7a; Library prepared by
 Edge Biosystems."

FEATURES

source
 1..27
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2847159"
 /tissue_type="Burkitt lymphoma"
 /cell_line="MGC4"
 /clone_lib="NIH_MGC_3"
 /note="Organ: Lymph; Vector: pOTB7a; Library prepared by
 Edge Biosystems."

Query Match 0.3%; Score 21.8; DB 1; Length 27;
 Best Local Similarity 92.0%; Pred. No. 1.8e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTCCTT 4488
 Db 27 TTTT...TTTTCCTT 3

RESULT 112

LOCUS CF291968
 DEFINITION 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
 sativa cDNA clone 14ROOT--02-J21, mRNA sequence.

ACCESSION CF291968
 VERSION CF291968.1 GI:33661001
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongui University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..27
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--02-J21"
 /tissue_type="root"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH108"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: pCR4-TORO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;

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Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 27 bp mRNA linear EST 15-AUG-2003
      ||||| 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
      1 TTTT... 4488
      |||||
      25

RESULT 113
CF3299084 LOCUS
DEFINITION 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION CF299084
VERSION CF299084.1 GI:33670845
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 27 bp mRNA linear EST 18-AUG-2003
      ||||| NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
      1 TTTT... 4488
      |||||
      25

RESULT 115
CF330557 LOCUS
DEFINITION NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-F04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 27 bp mRNA linear EST 18-AUG-2003
      ||||| NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
      3 TTTT... 725
      |||||
      27

RESULT 114
CF329725 LOCUS
DEFINITION NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF329725
VERSION CF329725.1 GI:33807665
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 27 bp mRNA linear EST 18-AUG-2003
      ||||| NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
      1 TTTT... 4488
      |||||
      25

RESULT 115
CF330557 LOCUS
DEFINITION NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--06-F04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 4488
Db 1 TTTT...TTT 25

RESULT 116
LOCUS CF335229 27 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--04-N08.bl ACJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--04-N08, mRNA sequence.
ACCESSION CF335229
VERSION CF335229.1 GI:33818810
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnah@gbio.com, bhnah@bio.myongji.ac.kr.

FEATURES
source
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/db_xref="GDB:3888877"
/db_xref="taxon:4530"
/clone="JMT--04-N08"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ACJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 4488
Db 1 TTTT...TTT 25

RESULT 117
LOCUS N29432 27 bp mRNA linear EST 05-JAN-1996
DEFINITION yw86h10-el Soares placenta 8to9weeks 2NbHP8to9w Homo sapiens cDNA
clone IMAGE:259171 3' similar to gb:X64559 TETRAECTIN PRECURSOR
(human); mRNA sequence.
ACCESSION N29432
VERSION N29432.1 GI:1147952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 4488
Db 2 TTTT...TTT 26

RESULT 118
LOCUS N52529 27 bp mRNA linear EST 15-FEB-1996
DEFINITION yv35a12-el Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone
IMAGE:244702 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
(HUMAN); mRNA sequence.
ACCESSION N52529
VERSION N52529.1 GI:1193695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

```

```

COMMENT      Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available royalty-free through LLNL ; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Trace considered overall poor quality
              Seq primer: m13 -40 forward
              High quality sequence stop: 1.
              Location/Qualifiers
FEATURES
    source
        1..27
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="GDB:3793948"
            /db_xref="taxon:9606"
            /clone="IMAGE:244702"
            /sex="male"
            /dev_stage="20 week-post conception fetus"
            /lab_host="DH10B (ampicillin resistant)"
            /clone_lib="Soares fetal liver spleen INFLS"
            /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
            with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
            1st strand cDNA was primed with a Pac I - oligo(dT) primer
            [5'-AACTGCAAGATTAATTAAGATCTTTTGTGCTTGA 3'],
            double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Pac I and cloned into the Pac I
            and Eco RI sites of the modified p773 vector. Library
            went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo."
Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4465 TTTTGTGCTGCTGA 4490
      |||||||
Db 1 TTTTGTGCTGCTGCTGA 26

RESULT 119
N89936 27 bp mRNA linear EST 02-APR-1996
LOCUS 2b23e12.s1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:302926 3' similar to GB:X59086 ATP SYNTHASE ALPHA CHAIN,
MITOCHONDRIAL PRECURSOR (HUMAN); mRNA sequence.
ACCESSION N89936
VERSION N89936.1 GI:1443263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ET primer
High quality sequence stop: 8.
Location/Qualifiers

source
    1..27
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0078H15"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

COMMENT      Contact: Wilson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0078 row: H column: 15
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 27.
              Location/Qualifiers
FEATURES
    source
        1..27
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0078H15"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

source
    1..27
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="GDB:1247858"
        /db_xref="taxon:9606"
        /clone="IMAGE:302926"
        /dev_stage="19 weeks"
        /lab_host="DH10B (ampicillin resistant)"
        /clone_lib="Soares fetal_lung_NbHL19W"
        /note="Organ: lung; Vector: p773D (Pharmacia) with a
        modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer
        [5'-TCCTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'],
        double-stranded cDNA was size selected, ligated to Eco RI
        adaptors (Pharmacia), digested with Not I and cloned into
        the Not I and Eco RI sites of a modified p773 vector
        (Pharmacia). Library went through one round of
        normalization to a Cot = 5. Library constructed by Bento
        Soares and M.Fatima Bonaldo. This library was constructed
        from the same fetus as the fetal heart library, Soares
        fetal heart NbHL19W."
Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGCTT 4488
      |||||||
Db 3 TTTTGTGCTGCTT 27

RESULT 120
AZ344642 27 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0078H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0078H15 R, genomic survey sequence.
ACCESSION AZ344642
VERSION AZ344642.1 GI:10423879
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Ayagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0078 row: H column: 15
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
FEATURES
    source
        1..27
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0078H15"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

```


/note=vector: PWD42nv; Purified genomic DNA from *M. musculus* C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
      |||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 25
      |||||

```

RESULT	122
AZ486791	
LOCUS	
DEFINITION	AZ486791 27 bp DNA linear GSS 05-OCT-2000 LM0315K21F Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0315K21 F, genomic survey sequence.

VERSION AZ486791.1 **GI:**10653911
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Becorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL *Genome Research*

COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Email: cdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: K column: 21
 Seq primer: CGTTGTAAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
 +
 /oranism="Mus musculus"
 source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315K21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pWP42nrv; Purified genomic DNA from M.

```


musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [G14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match          0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 4463 CTTTTTTTTTTTTTTTTTTTGGCT 4487
|||
Dp 3 CTTTTTTTTTTTTTTTTTTT 27

RESULT 131	TAJ55B06P/c	27 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	TAJ55B06P/c				
DEFINITION	T. brucei sheared genomic DNA clone 355b06, forward sequence, genomic survey sequence.				

AL493923
AL493923.1 GI:11870552
GSS.

SOURCE	ORGANISM
Trypanosoma brucei	Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	

REFERENCE
AUTHORS
TITLE
JOURNAL

1, (bases 1 to 27)
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R.,
Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L.,
Meville S.E., Rajandream M.A. and Barrell B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The $v + i$ method used for the library construction is described in detail in Smith, H. and Venter, J.C. (making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

FEATURES

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers

```

source
1. .27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="155b06"

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Query Match	0.3%	Score	21.8;	DB	1;	Length	27;
Best Local Similarity	92.0%	Pred. No.	1.8e+02;				
Matches	23;	Conservative	0;	Mismatches	2;	Indels	0;
						Gaps	0;

Oy	4464	TTTTTTTTTTTTTTTTTTTGTCTT	4488
nb	27	TTTTTTTTTTTTTTTTTTTTTTTTTT	3

RESULT	28 bp	linear	EST
132			14-AUG-2003
CF282351			
LOCUS			
CF282351			

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1				
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FEATURES
SOURCE

Query Match
Best Local
Matches

QY Db

RESULT 133
CF321885
LOCUS
DEFINITION

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE	TITLE
AUTHORS	JOURNAL
	COMMENT
1	
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FEATURES

14ETL--09-N05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
CF282351
CF282351.1 GI:33659738
EST.

Oryza sativa
Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Emaritoidae; Oryzaceae; *Oryza*.
 1 (bases 1 to 28)
 Kim, J. S., Jun, K. N., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
 Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahn@qbio.com, bnhahn@bio.myongji.ac.kr.

```

Location/Qualifiers
1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL-09-N05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for

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RT-PCR. " 0.3%; Score 21.8; DB 1; Length 28;
Similarity 92.0%; Pred. No. 2s+02;
23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 TTTT...TTTTTTTGTCCT 4488
1 TTTT...TTTTTTT 25

CF321885 28 bp mRNA linear EST 15-AUG-2003
HD--13-E16.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) *Oryza sativa* cDNA clone HD--13-E16, mRNA sequence.
CF321885
CF321885.1 GI:33693646
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Orvzeae; *Oryza*.

1. (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: N column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source

1. 28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0165N04"
/sex="Male"
/lab_host="B. Coli strain"
/clone_lib="Mouse 10kb p
/note="Vector: PWD42nv;
musculus C57BL/6J (male)
Laboratory Mouse DNA Res
(<http://www.jax.org/reso>
was hydrodynamically shea
0.005 inch orifice at co
was blunt end-repaired w
polynucleotide kinase. A
ligated to the blunt end
adaptor DNA was purifi
10.5 kb range using prep
electrophoresis. Vector
of PWD42 (gi_47321114|gb|
of inducible derivative of
with adaptors complement
purified. The sheared, a
adapted vector DNA, an
chemically-competent E.
and selected for ampicil

```
Query Match          0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 4464 TTTTIIITTTTTTTTTTTTTTTGTCCT 4488
 |||
DB 1 TTTTTTTTTTTTTTTTTTTTTTTTTT 25

RESULT 137
AZ401766/C

LOCUS	AZ401766	28 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	U061680ORC Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0168008 R, genomic survey sequence.				
ACCESSION	AZ401766				
VERSION	A2401766.1				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokess,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah				

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0168 row: 0 column: 08
Seq primer: CACACAGGAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source

1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0168008"
/sex="Male"
/lab_host="E. Coli strain"
/clone_lib="Mouse 10kb phage"
/note="Vector: PWD42nv;
musculus C57BL/6J (male)
Laboratory Mouse DNA Resource
(http://www.jax.org/resources)
was hydrodynamically sheared
0.005 inch orifice at constant
was blunt end-repaired with
polynucleotide kinase. A
ligated to the blunt end of
adaptor DNA was purified
10.5 kb range using prepure
electrophoresis. Vector
of PWD42 (gi|4732114|gb|
inducible derivative of
with adaptors complemented
purified. The sheared, and
adapted vector DNA, and
chemically-competent E. coli
and selected for ampicillin

```
Query Match      0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 4464 TTTTIIITTTTTTTTTTTTTTTGTCCTT 4488
 |||
pb 28 TTTTIIITTTTTTTTTTTTTTTT 4

RESULT 138
AZ471744

LOCUS	AZ471744	28 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	1M0286K08R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM0286K08 R, genomic survey sequence.				
ACCESSION	AZ471744				
VERSION	AZ471744.1	GI:10629965			
KEYWORDS	GSS.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.:Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT				

FEATURES

`/sex="Male"`
`/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"`
`/clone_lib="Mouse 10kb plasmid UUC1M library"`
`/notes="Vector: pWD42n; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource`
`(http://www.jax.org/resources/documents/dnares/). The DNA`
`was hydrodynamically sheared by repeated passage through a`
`0.005 inch orifice at constant velocity. The sheared DNA`
`was blunt end-repaired with T4 DNA polymerase and T4`
`polynucleotide kinase. Adaptor oligonucleotides were`
`ligated to the blunt ends in high molar excess. The`
`adapted DNA was purified and size-selected for a 9.5 to`
`10.5 kb range using preparative agarose gel`
`electrophoresis. Vector DNA was prepared from a derivative`
`of pWD42 (g14732114[gb|AF129072.1], a copy-number`
`inducible derivative of plasmid R1). The vector was ligated`
`with adaptors complementary to the insert adaptors and`
`purified. The sheared, adapted mouse DNA was annealed to`
`adapted vector DNA, and transformed into`
`chemically-competent E. coli XL10-Gold (Stratagene) cells`
`and selected for ampicillin resistance."`

Query Match : 0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2+02;
Matches 23; Conservative 0; Mismatches 2 Indels
and selected for ampicillin resistance.

	Qy	4464	TTTTTTTTTTTTTTTTTTTGTCTT	4488
b6		1	TTTTTTTTTTTTTTTTTTTTTTTTTT	25

RESULT 139

Accession	LOCUS	DEFINITION	AZ481286	28 bp DNA	linear	GSS 04-OCT-2000
AZ481286			IM0303L24F Mouse 10kb plasmid UGCG1M library			
			clone UGCG1M0303L24 F, genomic survey sequence.			

clone UUGC1M0303L24 F, 100%
ACCESSION AZ481286
VERSION AZ481286.1 GI:10642351

VERSION

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D. Weiss, R.

1 (bases 1 to 28)

Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Mus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE
Niederhauersen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

University of Utah Genome Center

University of
PA 300 PARML. 306, B1
84112. IISA

High quality sequence stop: 28.

FEATURES

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1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0177B08"
/sex="Male"
```

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/Clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1, the vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23; Conservative 0; Mismatches 2; Indels

Qy

4464 TTTTITTTTTTTTTTGTCCT 4488
|||||
pB

1 TTTTITTTTTTTTTTTTTTTTTT 25
|||||

RESULT 147
TA291A010/C

TA291A01Q 28 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 291a01, reverse sequence,
genomic survey sequence.
ACCESSION
AL486613
AL486613.1 GI:11853602
KEYWORDS
GSS

SOURCE
ORGANISM

ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE

AUTHORS	TITLE
Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajandream, M. A. and Barrell, B. G.	Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrel@sanger.ac.uk and nh@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TR9U27/4 Gurat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The λ vector used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

```

1. .28
location/Qualifiers
    /organism="Trypanosoma brucei"
    /mol_type="genomic DNA"
    /strain="TREU927"
    /db_xref="taxon:5691"
    /clone="291a01"

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```
.Query Match      0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23: Conservative 0; Mismatches 2; Indels
```

Qy 4464 TTTTITTTTTTTTTTTTGGCTT 4488
|||||
pB 28 TTTTITTTTTTTTTTTTTTTTTTTT 4
|||||

RESULT 148
TA379D11P

LOCUS	TR379D11P	28 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 379d11, forward sequence, genomic survey sequence				

genome survey sequences

ACCESSION	AL497637
VERSION	AL497637.1
GI	11873359

KEYWORDS
AD43
GSS.

RECORDS	SOURCE	ORGANISM
1
2
3
4
5
6
7
8
9
10
11
12
13
14
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18
19
20
21
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80
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82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

Organism
Trypanosoma Brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE
AUTHORS
1 (bases 1 to 28)
Hall, N. Rowman S.
trypanosoma.

ROBINSON
HARR, N., BOWMAN, S., DENMARD, N. O., DOGGSETT, J., ACKLIN, R.,
CHILLINGWORTH, C., ORMOND, D., HARRIS, B., EL-SAYED, N., HOU, L.,
MELVILLE, S. E., RATANDREAM, M. A., AND BARRELL, B. G.

TITLE	Direct Submission	Revised, D.E., RA, or Direct Submission
1. TITLE		
2. AUTHOR(S)		
3. ADDRESS		
4. CITY		
5. STATE		
6. ZIP		
7. COUNTRY		
8. PHONE		
9. FAX		
10. E-MAIL		
11. KEYWORDS		
12. ABSTRACT		
13. SUMMARY		
14. REFERENCES		
15. COMMENTS		

JOURNAL

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhi@sanger.ac.uk

COMMENT

Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The $v + i$ method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrel, Oxford University Press, 1999).

Details of T. brucei sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/projects/Tbrucei/>.

FEATURES
source

```

1. 20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="379d11"

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Query Match 0.3%; Score 21.8; DB 1; Length 28;
Best Local Similarity 92.0%; Pred. No. 2e+02;
Matches 23: Conservative 0; Mismatches 2; Indels

[illegible]

RESULT 149
CF279536

CF279536	29 bp	mRNA	linear	EST 14-AUG-2003
LOCUS				
DEFINITION	14ETL--05-N22.g1	Rice etiolated leaf	plasmid cDNA library (14ETL)	
ACCESSION	Oryza sativa cDNA clone 14ETL--05-N22	mRNA	sequence.	
	CF279536			


```

clone UUGC1M0281G24 F, genomic survey sequence.
AZ468402
VERSION
AZ468402.1 GI:10626527
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,K., Rose,R., Stokes,R., flngey,A., von
Niederhausern,A. and Wright,D.Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: G column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers

```

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1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0281G24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi:4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 2,1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTGCTT 4488
|||||
|||||
1 TTTTTTTTTTTTTTTTTTTTTT 25

Db

```

LOCUS	AZ486793	29 bp	DNA	linear	GSS 05-OCT-2000
DEFINITION	1M0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315N21 F, genomic survey sequence.				

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 29)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0180 row: L column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
which quality sequence stop: 29.

Location/Qualifiers
1. .29

```
/organism="Hae mab"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="TUGC2M0180L02"
 /sex="Male"
 /lab_host="E. Coli strain XL10 Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb Plasmid UUC1m library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnarses/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed into adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold ("Stratagene) cells and selected for ampicillin resistance."

0.3%	Score	21.8
92.0%	Pred. No.	

conservative 0; mismatch 4488

4480

TITLES

90 29 bp

9Q
ei sheared genomic DNA cl
currey sequence.

8 survey sequence.

8.1 GI:11868238

osoma brucei
osoma brucei

Protozoa; Euglenozoa; Kinetoplastida


```

Query Match      0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 2.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY   4464 TTTT...TTTTTTTGTCTT 4488
DB    25 TTTT...TTTTTTTGTCTT 4488

RESULT 173
AZ455741/c
LOCUS       AZ455741        30 bp     DNA             linear          GSS 04-OCT-2000
DEFINITION  IM0358D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0258D16 F, genomic survey sequence.
ACCESSION   AZ455741
VERSION     AZ455741.1 GI:10613866
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 30)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0258 row: D column: 16
Seq primer: CGTTGTAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0258D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES             source
1..30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0258D16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Best Local Similarity 92.0%; Pred. No. 2.3e+02; Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTGTCTT 4488
 Db 1 TTTT...TTTGTCTT 25

RESULT 175
 AZ582114
 LOCUS 1M0374J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M0374J17 F, genomic survey sequence.

ACCESSION AZ582114
 VERSION AZ582114.1 GI:11700674

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 30)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

Unpublished (2000)

JOURNAL

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0374 row: J column: 17

Seq primer: CTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0374J17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.3%; Score 21.8; DB 1; Length 30;
 Best Local Similarity 92.0%; Pred. No. 2.3e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTGTCTT 4488
 Db 1 TTTT...TTTGTCTT 25

RESULT 176

AZ249485

LOCUS

DEFINITION

2821429.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821429 3',

mRNA sequence.

ACCESSION AW249485

VERSION AW249485.1 GI:6592478

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2821429.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

Project Clone Distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 20

Contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 31 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this cDNA insert was

polyadenylated.

Plate: LiCM6 row: M column: 14

High quality sequence stop: 20.

Location/Qualifiers

1..31

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:2821429"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

ECORI; cDNA made by oligo-dT priming. Directionally

cloned into EcorI/XhoI sites using the following 5'

adaptor: GCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 21.8; DB 1; Length 31;
 Best Local Similarity 92.0%; Pred. No. 2.5e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTGTCTT 4488
 Db 4 TTTT...TTTGTCTT 28

```

RESULT 177
BX569502
LOCUS
DEFINITION BX569502 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse9a03_plc, mRNA sequence.
ACCESSION BX569502
VERSION BX569502.1 GI:33437420
KEYWORDS EST.
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 31)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..31
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/db_xref="taxon:37546"
/clone="Tse9a03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21.6; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 178
CF278807/c
LOCUS
DEFINITION CF278807 14ETL--04-N15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--04-N15, mRNA sequence.
ACCESSION CF278807
VERSION CF278807.1 GI:33656193
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 31)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..31
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--04-N15"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
|||||
Db 31 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 179
CF300345
LOCUS
DEFINITION CF300345 31 bp mRNA linear EST 15-AUG-2003
sativa cDNA clone 7LEAF--04-L08, mRNA sequence.
ACCESSION CF300345
VERSION CF300345.1 GI:33672106
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 31)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

REFERENCE
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..31
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--04-L08"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match

	Matches	23;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
Qy	4464	TTTTTTTTTTTTTTTTTTTTTTTTTTT	TGCTT	4488						
Dδ	31									
		TTTTTTTTTTTTTTTTTTTTTTTTTTT		7						

RESULT 182	AZ510092	31 bp	linear	GSS 05-OCT-2000
AZ510092/c	1W0354P14F	Mouse 10kb plasmid	UGCLM library	Mus musculus genomic
LOCUS	clone UGCLM0354P14 F,	genomic survey sequence.		
DEFINITION	AZ510092			
ACCESSION	AZ510092.1	GI:10691408		
VERSION	GSS.			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;			
REFERENCE	1 (bases 1 to 31)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Iqbal,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0354 row: P column: 14 Seq primer: CGTGTAAACGACGGCCAGT Class: plasmid ends High quality sequence stop: 31.			

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FEATURES
source
1..31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0354P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCM library"
/notes="vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (G14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match          0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Query Match	0.3%	Score	21.8;	DB	1;	Length	31;
Best Local Similarity	92.0%;	Pred. No.	2.5e+02;				
Matches	23;	Conservative	0;	Mismatches	2;	Indels	0;
						Gaps	0;

QY 4464 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCCTT 4488
Db 31 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 7

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RESULT 183
AZ623538
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

AZ623538 31 bp DNA linear GSS 13-DEC-2000
 1M0461G21F Mouse 10kb plasmid UGCLIM library Mus musculus genomic
 clone UGCLIM0461G21 F, genomic survey sequence.
 AZ623538
 AZ623538.1 GI:11745728
 GSS.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, W., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0461 row: G column: 21
 Seq primer: CGTTGTAACACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.

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FEATURES
source
Location/Qualifiers
1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0461G21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Query Match	0.3%	Score 21.8;	DB 1;	Length 31;
Best Local Similarity	92.0%;	Pred. No. 2.5e+02;		
Matches 23;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;


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Db      31 TTTTXXXXXXXXXXXXXXXXXXXXX

RESULT 186
AZ821215/c
LOCUS   AZ821215.1 31 bp DNA linear GSS 20-FEB-2001
DEFINITION
clone UUCG2M0093F21 R, genomic survey sequence.
ACCESSION
VERSION  AZ821215
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0093 row: F column: 21
          Seq primer: CACACAGGAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 31.
FEATURES             source
     Location/Qualifiers
         1..31
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUCG2M0093F21"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUCG1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adapted DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
                  inducible derivative of plasmid RI. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adapted mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."
Query Match       0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred.No.2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTGTCCT 4488
Db      31 TTTTXXXXXXXXXXXXXXXXXXXXX

RESULT 187
AZ826618/c
LOCUS   AZ826618.1 31 bp DNA linear GSS 20-FEB-2001
DEFINITION
clone UUCG2M0102C19 F, genomic survey sequence.
ACCESSION
VERSION  AZ826618
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0102 row: C column: 19
          Seq primer: CGTTGTAAACGACGCCAGT
          Class: plasmid ends
          High quality sequence stop: 31.
FEATURES             source
     Location/Qualifiers
         1..31
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUCG2M0102C19"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUCG1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
                  musculus C57BL/6J (male) was obtained from the Jackson
                  Laboratory Mouse DNA Resource
                  (http://www.jax.org/resources/documents/dnares/). The DNA
                  was hydrodynamically sheared by repeated passage through a
                  0.005 inch orifice at constant velocity. The sheared DNA
                  was blunt end-repaired with T4 DNA polymerase and T4
                  polynucleotide kinase. Adaptor oligonucleotides were
                  ligated to the blunt ends in high molar excess. The
                  adapted DNA was purified and size-selected for a 9.5 to
                  10.5 kb range using preparative agarose gel
                  electrophoresis. Vector DNA was prepared from a derivative
                  of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
                  inducible derivative of plasmid RI. The vector was ligated
                  with adaptors complementary to the insert adaptors and
                  purified. The sheared, adapted mouse DNA was annealed to
                  adaptor vector DNA, and transformed into
                  chemically-competent E. coli XL10-Gold (Stratagene) cells
                  and selected for ampicillin resistance."
Query Match       0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred.No.2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTGTCCT 4488
Db      31 TTTTXXXXXXXXXXXXXXXXXXXXX

```

```

RESULT 188
TA244G08P      31 bp  DNA  linear  GSS 13-DEC-2000
LOCUS          T. brucei sheared genomic DNA clone 244G08, forward sequence,
DEFINITION     genomic survey sequence.
ACCESSION      AL483539
VERSION        AL483539.1 GI:11849040
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
               Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
               Trypanosoma.
REFERENCE      1 (bases 1 to 31)
AUTHORS       Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
               Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
               Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE         Direct Submission
JOURNAL        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
               project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
               Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
               nh@sanger.ac.uk
COMMENT        Constructed at the Institute for Genomic Research (TIGR),
               Rockville, MD. Genomic DNA isolated from a cloned population of
               Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
               to give a tight size distribution (
               4 kb). The v + i method used for the library construction is
               described in detail in Smith, H. and Venter, J.C. (Making small
               insert libraries for whole genome shotgun sequencing projects. In
               Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
               Barrell, Oxford University Press, 1999).
               Email: nelsayed@igr.org
               Details of T. brucei sequencing at the Sanger Centre are available
               at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES       Location/Qualifiers
               1..31
               /organism="Trypanosoma brucei"
               /mol_type="genomic DNA"
               /strain="TREU927"
               /db_xref="taxon:5691"
               /clone="244G08"
Query Match      0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 189
AW327277/C     32 bp  mRNA  linear  EST 28-JAN-2000
LOCUS          GQ10D07.X1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846628 5', mRNA
DEFINITION     sequence.
ACCESSION      AW327277
VERSION        AW327277.1 GI:6797772
KEYWORDS       EST.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 32)
AUTHORS       NIH-MGC http://mgi.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL        Unpublished (1999)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cga@bpe-remail.nih.gov
               Tissue Procurement: ATCC
               cDNA Library Preparation: Edge Biosystems
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: NIH Intramural Sequencing Center (NISC)
FEATURES       Location/Qualifiers
               1..32
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="IMAGE:4670136"
               /tissue_type="adenocarcinoma"
               /lab_host="DH10B (TI phage-resistant)"
               /clone_lib="NIH_MGC_60"
               /notes="Organ: prostate; Vector: pDNR-LIB (Clontech);
               Site1: SfiI (ggccgctcgcc); Site2: SfiI
               (ggccattatggcc); Double-stranded cDNA was prepared from
               cell line RNA. 5' and 3' adaptors were used in cloning as
               follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
               3' adaptor sequence:
               5'-ATTCTAGAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,
               C, or G and N = A, C, G, or T). Average insert size 1.5
               kb (range 0.9-4.0 kb). 14/15 colonies contained inserts
               by PCR. This library was enriched for full-length clones
               and was constructed by Clontech Laboratories (Palo Alto,

```

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Plate: LLCM0028 row: G column: 13
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..32
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2846628"
 /tissue_type="T cell leukemia"
 /cell_line="MGC2"
 /clone_lib="NIH_MGC_2"
 /note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

FEATURES source

Query Match 0.3%; Score 21.8; DB 1; Length 32;
 Best Local Similarity 92.0%; Pred. No. 2.7e+02;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
 |||||

Db 32 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 190

LOCUS BG501238/c

DEFINITION BG501238 32 bp mRNA linear EST 27-MAR-2001
 mRNA sequence.
 ACCESSION BG501238
 VERSION BG501238.1 GI:13462755
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 32)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cga@bpe-remail.nih.gov
 Tissue Procurement: DCTD/DTT
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM1483 row: C column: 01
 High quality sequence stop: 32.

FEATURES source

Location/Qualifiers

1..32

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4670136"

/tissue_type="adenocarcinoma"

/lab_host="DH10B (TI phage-resistant)"

/clone_lib="NIH_MGC_60"

/notes="Organ: prostate; Vector: pDNR-LIB (Clontech);

Site1: SfiI (ggccgctcgcc); Site2: SfiI

(ggccattatggcc); Double-stranded cDNA was prepared from

cell line RNA. 5' and 3' adaptors were used in cloning as

follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and

3' adaptor sequence:

5'-ATTCTAGAGCGGCGGCGGCACATG-dT(30)BN-3' (where B = A,

C, or G and N = A, C, G, or T). Average insert size 1.5

kb (range 0.9-4.0 kb). 14/15 colonies contained inserts

by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto,

CA). Note: this is a NIH_MGC Library."

Query Match 0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTTCTTTTCTTTTCTTTG 4489
DB 32 TTTTCTTTTCTTTTCTTTG 8

RESULT 191
CF291773
LOCUS CF291773 32 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-F12, mRNA sequence.
ACCESSION CF291773
VERSION CF291773.1 GI:33660806
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 32)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTG 4488
DB 1 TTTTCTTTTCTTTTCTTTT 25

RESULT 192
CF299386
LOCUS CF299386 32 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-G07, mRNA sequence.
ACCESSION CF299386
VERSION CF299386.1 GI:33671147
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 32)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTG 4488
DB 1 TTTTCTTTTCTTTTCTTTT 25

RESULT 193
CF309233/c
LOCUS CF309233 32 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-F14, mRNA sequence.
ACCESSION CF309233
VERSION CF309233.1 GI:33680994
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 32)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

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/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"


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/lab_host="E.coli DH108"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 197
CF321046
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
Song,S.I., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Kim,J.S., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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/organism="Oryza sativa"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 199
CF331270
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 32
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/clone="HD--12-C15"
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/lab_host="E.coli DH108"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

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|||||
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RESULT 198
CF328471
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 32
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-G09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 199
CF331270
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 32
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 199
CF331270
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 32
/organism="Oryza sativa"
/mol_type="mRNA"
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/clone="NACL--03-G09"
/tissue_type="callus"
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/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

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All clones with suffix qic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

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Query Match      0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACTTTTTCCTTTTTCCTTC 4486
Db 9 AGTTTTTTTTTTTTTTTTTTTC 33

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RESULT 207
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LOCUS
DEFINITION
  14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
  sativa cDNA clone 14ROOT--02-B21, mRNA sequence.
ACCESSION
CF291613
VERSION
CF291613.1 GI:33660646
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 33)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
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      for 2hrs. Oligo-capped mRNA was reverse transcribed and
      then used for PCR. mRNA was prepared from ABA-responsive
      element binding transcription factor 3 overexpression
      line."

Query Match      0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTCCTTC 4488
Db 1 TTTTTCCTTTTTCCTTCCTTC 25

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FEATURES
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      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTCCTTC 4488
Db 1 TTTTTCCTTTTTCCTTCCTTC 25

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RESULT 208
CF311229
LOCUS
DEFINITION
  ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA
  library (ABF) Oryza sativa cDNA clone ABF--06-F23, mRNA sequence.
ACCESSION
CF311229
VERSION
CF311229.1 GI:33682990
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 33)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
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      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="ABF--06-F23"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="ABF3-overexpressing transgenic rice plasmid
      cDNA library (ABF)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
      for 2hrs. Oligo-capped mRNA was reverse transcribed and
      then used for PCR. mRNA was prepared from ABA-responsive
      element binding transcription factor 3 overexpression
      line."

Query Match      0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTCCTTC 4488
Db 1 TTTTTCCTTTTTCCTTCCTTC 25

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FEATURES
source
  Location/Qualifiers
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      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="ABF--06-F23"
      /tissue_type="leaf"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="ABF3-overexpressing transgenic rice plasmid
      cDNA library (ABF)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
      for 2hrs. Oligo-capped mRNA was reverse transcribed and
      then used for PCR. mRNA was prepared from ABA-responsive
      element binding transcription factor 3 overexpression
      line."

Query Match      0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTCCTTC 4488
Db 1 TTTTTCCTTTTTCCTTCCTTC 25

RESULT 209
CF326967
LOCUS
DEFINITION
  NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
  sativa cDNA clone NACL--01-E04, mRNA sequence.
ACCESSION
CF326967
VERSION
CF326967.1 GI:33802189
KEYWORDS
EST.
SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 33)
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

FEATURES
source
  Location/Qualifiers
    1..33
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="14ROOT--02-B21"
      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 33;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTCCTTC 4488
Db 1 TTTTTCCTTTTTCCTTCCTTC 25

```

of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
E-mail: myongji.ac.kr.

FEATURES

```

1. 33
   /organism="Oryza sativa"
   /mol_type="mRNA"
   /cultivar="Nackdong"
   /db_xref="taxon:4530"
   /clone="NACL-01-E04"
   /issue_type="callus"
   /tissue_type="callus"
   /dev_stage="proliferated callus on 2N6 media for 30 days"
   /lab_host="E.coli DH10B"
   /clone_lib="Rice callus plasmid cDNA library (NACL)"
   /notes="Rice callus mRNA was capped
   with oligobionucleotides and then used as templates for
   RT-PCR."

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```

Query Match          0.3%; Score 21.6; D2 2;
Best Local Similarity 92.0%; Pred. No. 2.9e+02; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 2;

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QY

4464 TTTTTTTTTTTTTTTTTTTTTTTT 25
|||||

Dd

1 TTTTTTTTTTTTTTTTTTTTTTTT 25
|||||

RESULT 210	33 bp	mRNA	linear	EST 18-AUG-2003
CF328313/c				
LOCUS	CF328313			
DEFINITION	NACL--03-C14.g1	Rice callus plasmid cDNA library	(NACL) Oryza	
FEATURES				
ORIGIN				
COMMENTS				

ACCESSION
CF328313
CT.33804873

VERG. EST.
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Gramineae; Oryza.

REFERENCE
1. (bases 1 to 33)
Ehrhartoidae; *Oryzaceae*, *Oryza* sp.
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C.,
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)

Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H., GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, Seoul, University

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhahmeggbio.com, bhahmeggbio.myongji.ac.kr.
bhahmeggbio@yongin.ac.kr

FEATURES

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1. 33
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL-03-C14"
/cisue_type="callus"
/dev_stage="proliferated"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cdna library (NACL)"
/notes="Vector: pK41-ROB; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match          0.3%;   Score 21.8;   DB 1;   Length 33;
Best Local Similarity 92.0%;   Pred. No. 2.9e+02;
Matches 23;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

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4464 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTCTT 4488
33 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 9

RESULT 211

CF336752 33 bp mRNA linear ES1 18-AUG 2001

ACCESSION
CF336752
Library (UMI) 01221884

EST.
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Tracheophyta; Poaceae; Oryza.

REFERENCE
AUTHORS
1 (bases 1 to 33)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, I. C.,
Kim, Y.-K., Kim, Y.-K. and Nahm, B. H.
Song, S. I., Kim, J. K., Kim, Y.-K. and Lee, T. H.
Ministry of Agriculture and Forestry, Republic of Korea
1990. Rice Production Statistics, Seoul, Korea.

TITLE Large-scale Sequencing Analysis of the Human Genome
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Bioinformatics, Myongji University
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio. myongji. ac. kr.

FEATURES

```

1. 33
  organism="Oryza sativa"
  mol_type="mRNA"
  cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="JMT--06-019"
  /issue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="AtJMT-overexpressing transgenic rice plasmid
  cDNA library (JMT)"
  /notes="Vector: pCR4-TOPO; site 1: EcoRI; Oligo-capped mRNA
  was reverse transcribed and then used for PCR. mRNA was
  generated from Arabidopsis Jasmonate Carboxyl
  transferase cDNA library."

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Query Match	0.3%	Score 21.0;	0;	Gaps	0;
Best Local Similarity	92.0%	Pred. NO. 2.9e+02;		Indels	
Best Local Similarity	92.0%	0; Mismatches	2;		
Conservative	92.0%	0; Mismatches	2;		

[illegible]

RESULT 212

RESULT 212					EST 18-AUG-2003
CF337105		linear	33 bp	mRNA	
CF337105		transgenic rice plasmid cDNA			
LOCUS	CF337105	atTMT-overexpressing transgenic rice			
					mRNA sequence.

ACCESSION	CF337105	GT:33822596

EST. Oryza sativa
SOURCE Streptophyta; Embryophyta; Tracheophyta;
ORGANISM Eukaryota; Viridiplantae; Poales; Poaceae;
Liliopsida; Magnoliophyta; Magnoliopsida;
Spermatophyta; Magnoliopsida; Poales; Poaceae;
Oryza.

REFERENCE

Ehrhardtoidae; Oryzae, p. 33
1 (bases 1 to 33)

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs

TITLE

```

Query Match          0.3%; Score 22.7;
Best Local Similarity 92.0%; Pred. No. 2.9e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```



```

Qy 4464 TTTT...TTTGTGTC 4486
Db 2 TTTT...TTTTC 24

RESULT 224
AL587582 27 bp DNA linear GSS 26-APR-2001
LOCUS 2M0201004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0201004 R, genomic survey sequence.
ACCESSION AL587582
VERSION AL587582.1 GI:13804440
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: 0 column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0201004"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTGTGTC 4486
Db 2 TTTT...TTTTC 24

RESULT 224
AL587582 27 bp DNA linear GSS 26-APR-2001
LOCUS 2M0201004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0201004 R, genomic survey sequence.
ACCESSION AL587582
VERSION AL587582.1 GI:13804440
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: 0 column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
Location/Qualifiers
1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0201004"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 4463 CTTT...TTTGTGTC 4485
Db 4 CTTT...TTTTC 26

RESULT 225
AL587582 28 bp mRNA linear EST 02-MAR-2001
LOCUS AL587582 BP Chicken Brain Library Gallus gallus cDNA clone
DEFINITION ROS059D03, mRNA sequence.
ACCESSION AL587582
VERSION AL587582.1 GI:13192616
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 28)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GGCGCGCTTTT...TTTTC 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
FEATURES
Location/Qualifiers
1..28
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="ROS059D03"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
5' TCACCTCTGAG 3' ; 3' adaptor sequence: 5'
GGCGCGCTTTT...TTTTC 3' Poly A RNA purchased from
Clontech (*6854-1)"

Query Match 0.3%; Score 21.4; DB 1; Length 28;
Best Local Similarity 95.7%; Pred. No. 2.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTGTGTC 4486
Db 6 TTTT...TTTTC 28

RESULT 226
AL048684/c 30 bp mRNA linear EST 04-SEP-2003
LOCUS AL048684 r1 566 (synonym: hfkcd2) Homo sapiens cDNA clone
DEFINITION DXF2p566C043, mRNA sequence.
ACCESSION AL048684
VERSION AL048684.1 GI:4727755
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 30)
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehler, et al.)
Unpublished (1999)

```

```

COMMENT      Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566C043"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.3%; Score 21.4; DB 1; Length 30;
Best Local Similarity 95.7%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGAGTCTTTTGTGTC 4486
Db 30 TTTTGTGCTGAGTCTTTTGTGTC 8

RESULT 227
AL048732/c
LOCUS      AL048732      30 bp      mRNA      linear      EST 04-SEP-2003
DEFINITION DKFZp566I053_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION  AL048732
VERSION     AL048732.1 GI:4727803
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 30)
AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE     EST (Koehrer, et al.)
JOURNAL   Unpublished (1999)
COMMENT   Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566I053"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.3%; Score 21.4; DB 1; Length 30;
Best Local Similarity 95.7%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGAGTCTTTTGTGTC 4486
Db 30 TTTTGTGCTGAGTCTTTTGTGTC 8

RESULT 228
AV966771
LOCUS      AV966771      31 bp      mRNA      linear      EST 14-MAR-2002
DEFINITION AV966771 Nori Satoh unpublished cDNA library, young adult Ciona
ACCESSION  AV966771
VERSION     AV966771.1 GI:19456467
KEYWORDS   EST.
SOURCE     Ciona intestinalis

COMMENT      Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1. .30
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566I053"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.3%; Score 21.4; DB 1; Length 30;
Best Local Similarity 95.7%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGCTGAGTCTTTTGTGTC 4486
Db 30 TTTTGTGCTGAGTCTTTTGTGTC 8

RESULT 229
BX557762
LOCUS      BX557762      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION BX557762 Glossina morsitans morsitans adult infected gut Glossina
ACCESSION  BX557762
VERSION     BX557762.1 GI:33428937
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans
REFERENCE  1 (bases 1 to 31)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
          Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hall N
          Pathogen Sequencing Unit
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix gic are reverse primer reads starting at 5'
          end of the cDNA all plc reads are from
          the 3' end.

FEATURES
source
1. .31
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"

ORGANISM      Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
REFERENCE  1 (bases 1 to 31)
AUTHORS   Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE     Expressed genes in Ciona intestinalis
JOURNAL   Unpublished (2000)
COMMENT   Contact: Nori Satoh
          Department of Zoology
          Kyoto University
          Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
          Tel: 81-75-753-4081
          Fax: 81-75-705-1113
          Email: satho@acidian.zool.kyoto-u.ac.jp.

FEATURES
source
1. .31
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciad18pl6"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
          adult"

Query Match      0.3%; Score 21.4; DB 1; Length 31;
Best Local Similarity 80.6%; Pred. No. 2.9e+02;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4452 GGTGGCATGGACTTTTTTTTTTTTTTTTTTTT 4482
Db 1 GCTAGTCTCGAGTTTTTTTTTTTTTTTTTTTTT 31

RESULT 229
BX557762
LOCUS      BX557762      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION BX557762 Glossina morsitans morsitans adult infected gut Glossina
ACCESSION  BX557762
VERSION     BX557762.1 GI:33428937
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans
REFERENCE  1 (bases 1 to 31)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
          Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hall N
          Pathogen Sequencing Unit
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix gic are reverse primer reads starting at 5'
          end of the cDNA all plc reads are from
          the 3' end.

FEATURES
source
1. .31
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"

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RESULT	232
LOCUS	BQ591183
DEFINITION	BQ591183 27 bp mRNA linear EST 06-DEC-2002 E012715-024-017-L16-T7 MPZ-ADIS-024-storage root Beta vulgaris
ACCESSION	CDNA clone 024-017-L16 3-PRIME, mRNA sequence.
VERSION	BQ591183
KEYWORDS	BQ591183.1 GI:26120766
SOURCE	EST.
ORGANISM	Beta vulgaris Beta vulgaris Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

```

REFERENCE
AUTHORS      1 (bases 1 to 27)
              Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,W., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PubMed      12472698
COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weissnae@mpiz-koeln.mpg.de
              Insert Length: 27 Std Error: 0.00
              Plate: 17 row: L column: 16
              Seq primer: T7; GTAATACGACTCACTATAGGC.

FEATURES
source       1..27
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:188934"
              /db_xref="taxon:161934"
              /clone="024-017-Li6"
              /tissue_type="storage root"
              /lab_host="EMDH10B"
              /clone_lib="MPIZ-ADIS-024-storage root"
              /notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
              orientation:
              SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 21.2; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 2.3e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4466 TTTTGTGTTTTTTTGTCTTGAG 4491
Db 1 TTTTGTGTTTTTTTGTCTTGAG 26

RESULT 233
R37697
LOCUS       R37697      28 bp      mRNA      linear      EST 04-MAY-1995
DEFINITION yf50c03.s1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:25521 3' similar to gb:J03040 SPARC PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION   R37697
VERSION     R37697.1 GI:795153
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine

Query Match      0.3%; Score 21.2; DB 1; Length 28;
Best Local Similarity 85.2%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4465 TTTTGTGTTTTTTTGTCTTGAG 4491
Db 1 TTTTGTGTTTTTTTGTCTTGAG 27

RESULT 234
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LOCUS       AZ358038/c 28 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION clone UUGC1M0100F05 F, genomic survey sequence.
ACCESSION   AZ358038
VERSION     AZ358038.1 GI:10471738
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0100 row: F column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1410
 High quality sequence starts: 1 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL This clone is available royalty-free
 through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
 for further information. Trace considered overall poor quality
 Insert Length: 1410 Std Error: 0.00
 Seq primer: -21ml3
 High quality sequence stop: 1.

FEATURES

source

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 /mol_type="mRNA"
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 /db_xref="taxon:9606"
 /clone="IMAGE:25521"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares infant brain INIB"
 /note="Organ: whole brain; Vector: Lfamid BA; Site 1: Not
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer [5,
 AACTGGAGAAATTCGGCGCGAGGAATTTTTTTTTTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lfamid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.3%; Score 21.2; DB 1; Length 28;
 Best Local Similarity 85.2%; Pred. No. 2.5e+02;
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 4465 TTTTGTGTTTTTTTGTCTTGAG 4491
 Db 1 TTTTGTGTTTTTTTGTCTTGAG 27

RESULT 234
 R37697
 LOCUS AZ358038/c 28 bp DNA linear GSS 02-OCT-2000
 DEFINITION clone UUGC1M0100F05 F, genomic survey sequence.
 ACCESSION AZ358038
 VERSION AZ358038.1 GI:10471738
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0100 row: F column: 05
 Seq primer: CGTTGTAAAACGACGGCCAGT

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Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0074C14"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1m library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 21.2; DB 1; Length 28;
Best Local Similarity 88.5%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTCT 4487
   |||||
Db 26 AATTTTCTTTTCTTTTCTTTTCT 1

RESULT 235
AZ809971
LOCUS      28 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0074C14F Mouse 10kb plasmid UUC1m library Mus musculus genomic clone UUC2M0074C14 F, genomic survey sequence.
ACCESSION  AZ809971
VERSION     AZ809971.1 GI:12976769
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: C column: 14
Seq primer: CGTTGTAACGACGGCAGT
Class: plasmid ends

Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0100F05"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1m library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 21.2; DB 1; Length 28;
Best Local Similarity 88.5%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTCT 4487
   |||||
Db 26 AATTTTCTTTTCTTTTCTTTTCT 1

RESULT 235
AZ809971
LOCUS      28 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0074C14F Mouse 10kb plasmid UUC1m library Mus musculus genomic clone UUC2M0074C14 F, genomic survey sequence.
ACCESSION  AZ809971
VERSION     AZ809971.1 GI:12976769
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Iellam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: C column: 14
Seq primer: CGTTGTAACGACGGCAGT
Class: plasmid ends

Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0074C14"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1m library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 21.2; DB 1; Length 28;
Best Local Similarity 88.5%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTCTTTTCTTTTCTTTTCT 4484
   |||||
Db 3 TTGCTTTTCTTTTCTTTTCTTTTCT 28

RESULT 236
AV959965
LOCUS      31 bp mRNA linear EST 14-MAR-2002
DEFINITION AV959965 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciadi4mi2 5', mRNA sequence.
ACCESSION  AV959965
VERSION     AV959965.1 GI:19448264
KEYWORDS    EST.
SOURCE      Ciona intestinalis
ORGANISM    Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 31)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES
source
1. .31
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="ciadi4mi2"
/tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"

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Query Match      0.3%; Score 21.2; DB 1; Length 31;
Best Local Similarity 85.2%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTTGT 4485
DB 5 TCGAGTTTTTTTTTTTTTTTTTTTCGT 31

RESULT 237
BX551460 32 bp mRNA linear EST 10-OCT-2003
LOCUS
DEFINITION BX551460 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse118902_plc, mRNA sequence.
ACCESSION BX551460
VERSION
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse118902_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 85.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4460 GGACTTTTTTTTTTTTTTTTTTTTGT 4485
DB 6 GGTGCTTTTTTTTTTTTTTTTTTTT 31

RESULT 239
BX555533
LOCUS
DEFINITION BX555533 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21c01_plc, mRNA sequence.
ACCESSION BX555533
VERSION BX555533.1 GI:33379519
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit

```

```

EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
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response genes
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Hinxton, Cambridge, CB10 1SA, UK
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse118902_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 88.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4460 GGACTTTTTTTTTTTTTTTTTTTTGT 4485
DB 6 GGTGCTTTTTTTTTTTTTTTTTTTT 31

RESULT 239
BX555533
LOCUS
DEFINITION BX555533 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21c01_plc, mRNA sequence.
ACCESSION BX555533
VERSION BX555533.1 GI:33379519
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
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COMMENT Contact: Hall N
Pathogen Sequencing Unit

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Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1..32 Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse21c01_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 88.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTG 4484
Db 4 TAGAAGTTTTTTTTTTTTTTTTTTG 29

RESULT 240
BX558102
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 32)
Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
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morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

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University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1..32 Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse36f08_plc"

/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 88.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4458 ATGACATTTTTTTTTTTTTTTTTTTT 4483
Db 7 ATAGTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 241
BX560723
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 32)
Lehane,M.J., Aksoy,S., Gibson,W., Keshornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1..32 Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse50g08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 88.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4458 ATGACATTTTTTTTTTTTTTTTTTTT 4483
Db 7 ATAGTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 242
BX564047

[illegible]

```

RESULT 250
BH000233/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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FEATURES
source
high quality sequence stop: 22.
Location/Qualifiers
1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0287L21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G[4732114]gb/AP129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.3%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels

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QY      4463 CTTTTTTTTTTTTTTTTTTT 4483
Db      21 CTTTTTTTTTTTTTTTTTTT 1

RESULT 251
LOCUS   AZ315640/c
DEFINITION AZ315640 23 bp DNA linear GSS 29-SEP-2000
ACCESSION IM0033004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION    clone UUGC1M0033004 F, genomic survey sequence.
KEYWORDS   AZ315640
SOURCE     AZ315640.1 GI:10362861
ORGANISM   GSS.
           Mus musculus (house mouse)

REFERENCE 1 (bases 1 to 23)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
           1 (bases 1 to 23)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
           Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
           Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
           Niederhausern,A. and Wright,D.,Weiss,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
           Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT   University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0033 row: 0 column: 04
           Seq primer: CGTTGTAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 23.
FEATURES
    source
    1..23
        Location/Qualifiers
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0033004"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="Vector: pWD42nv, Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match 0.3%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTTTTG 4484
Db      23 TTTTTTTTTTTTTTTTTTTG 3

RESULT 252
LOCUS   CF326993/c
DEFINITION CF326993 24 bp mRNA linear EST 18-AUG-2003
ACCESSION NACL--01-E17.g1 Rice callus plasmid cDNA library (NACL) Oryza
VERSION    sativa cDNA clone NACL--01-E17, mRNA sequence.
KEYWORDS   CF326993.1 GI:33802241
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
           1 (bases 1 to 24)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
           Large-scale Sequencing Analysis of Rice ESTs
           Unpublished (2003)
JOURNAL   Contact: Nahm B.H.
COMMENT   Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
    source
    1..24
        Location/Qualifiers
            /organism="Oryza sativa"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:4530"
            /clone="NACL-01-E17"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 30 days"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice callus plasmid cDNA library (NACL)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
            with oligoribonucleotides and then used as templates for
            RT-PCR."
Query Match 0.3%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTTTTG 4484
Db      22 TTTTTTTTTTTTTTTTTTTG 2

RESULT 253
LOCUS   AZ404871/c
DEFINITION AZ404871 24 bp DNA linear GSS 03-OCT-2000
ACCESSION IM0173014R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION    clone UUGC1M0173014 R, genomic survey sequence.
KEYWORDS   AZ404871
SOURCE     GSS.
           Mus musculus (house mouse)
           Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
           1 (bases 1 to 24)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
           Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
           Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
           Niederhausern,A. and Wright,D.,Weiss,R.
           Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
           Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
COMMENT   University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0033 row: 0 column: 04
           Seq primer: CGTTGTAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 23.
FEATURES
    source
    1..23
        Location/Qualifiers
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0033004"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /notes="Vector: pWD42nv, Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match 0.3%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
PUBMED	8889549
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence starts: 1 High quality sequence stops: 1 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: ml3 -40 forward High quality sequence stop: 1.
FEATURES	Location/Qualifiers source 1..25 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:3866115" /db_xref="taxon:9606" /clone="IMAGE:255706" /sex="Female" /tissue_type="olfactory epithelium" /lab_host="SOLR cells (kanamycin resistant)" /dev_stage="35 year old" /clone_lib="Weizmann Olfactory Epithelium" /note="Organ: nose; Vector: pBluescript SK-; Site_1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Olfactory epithelium, normal. Average insert size: 0.8 kb; Uni-ZAP XR vector. Library constructed by N. Walker, D. Lancet, Weizmann Institute of Science. ~5' adaptor sequence: 5' GAATTCGGCAGCG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"
Query Match	0.3%; Score 21; DB 1; Length 25;
Best Local Similarity	100.0%; Pred. No. 2.1e+02;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	4464 TTTTNTTTTTTTTTTTTTTG 4484 TTTTTTTTTTTTTTT Db 2 TTTTNTTTTTTTTTTTTTTG 22
RESULT 256	
CG726337	
LOCUS	1119089E32.2ELy1 1119 - RescueMu Grid AA Zea mays genomic, genomic survey sequence.
DEFINITION	CG726337 25 bp DNA linear GSS 20-OCT-2003
ACCESSION	CG726337.1 GI:37764992
VERSION	GSS.
KEYWORDS	Zea
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 25) Walbot,V.
AUTHORS	Maize genomic sequences found using engineered RescueMu transposon
TITLE	Unpublished (2001)
JOURNAL	Contact: Walbot V
COMMENT	Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Possible ligation site of ends cut by 2 different endonucleases. Reverse complemented post-ligation sequence from source sequence.


```

/lab host="E.coli DH108"
/clone lib="rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21; DB 1; Length 29;
Best Local Similarity 82.8%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4466 TTTTCTTTTCTTTTCTTTGTCGAGACA 4494
      |||||
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTAAAAA 29

RESULT 261
CF314795
LOCUS
DEFINITION HD--03-H09_g1 OsHDA1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--03-H09, mRNA sequence.
ACCESSION CF314795
VERSION CF314795.1 GI:33686556
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..29
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--03-H09"
/tissue_type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OsHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCTTTTCTTTT 4483
      |||||
Db 1 CTTTCTTTTCTTTTCTTTTCTTTT 21

RESULT 262
BQ592535
LOCUS
DEFINITION BQ592535 30 bp mRNA linear EST 06-DEC-2002
vulgaris cDNA clone 024-028-B14 5-PRIME, mRNA sequence.
ACCESSION BQ592535

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```

BQ592535.1 GI:26122118
EST.
KEYWORDS Beta vulgaris
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 30)
AUTHORS Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radloff, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@piz-koeln.mpg.de
Insert length: 30 Std Error: 0.00
Plate: 28 row: B column: 14
Seq primer: SP6r; ATTTAGTGACACTATAGAAGA.
Location/Qualifiers
1..30
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:194319"
/db_xref="taxon:161934"
/clone="024-028-B14"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-developing root"
/notes="vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SALI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 21; DB 1; Length 30;
Best Local Similarity 82.8%; Pred. No. 3.2e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4452 GGTGGCATGACCTTTTCTTTTCTTTT 4480
      |||||
Db 2 GGACGCGTGGTCTTTTCTTTTCTTTT 30

RESULT 263
TA226G05P/c
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 226g05, forward sequence,
genomic survey sequence.
ACCESSION AL480085
VERSION AL480085.1 GI:11845964
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 30)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

```


Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse21g09_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTGTGCTTTTGTGCT 4484
|||||
Db 12 TTTTGTGCTTTTGTGCT 32
|||||

RESULT 270
BX555625
LOCUS
DEFINITION BX555625 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21g09_plc, mRNA sequence.
ACCESSION BX555625
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehan
Prof. M.J. Lehan
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse21g09_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTGTGCTTTTGTGCT 4484
|||||
Db 12 TTTTGTGCTTTTGTGCT 32
|||||

RESULT 270
BX555625
LOCUS
DEFINITION BX555625 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21g09_plc, mRNA sequence.
ACCESSION BX555625
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehan
Prof. M.J. Lehan
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse21g09_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4465 TTTTGTGCTTTTGTGCT 4485
|||||
Db 11 TTTTGTGCTTTTGTGCT 31
|||||

RESULT 272
BG670391/c
LOCUS
DEFINITION BG670391 Rat DRG Library Rattus norvegicus cDNA clone DRNBAF06 5',
mRNA sequence.

/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 82.8%; Pred. No. 3.7e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTGTGCT 4487
|||||
Db 4 TAGATAGTTTGTGCT 32
|||||

RESULT 271
BX557354
LOCUS
DEFINITION BX557354 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse31g07_plc, mRNA sequence.
ACCESSION BX557354
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehan
Prof. M.J. Lehan
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse31g07_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4465 TTTTGTGCTTTTGTGCT 4485
|||||
Db 11 TTTTGTGCTTTTGTGCT 31
|||||

RESULT 272
BG670391/c
LOCUS
DEFINITION BG670391 Rat DRG Library Rattus norvegicus cDNA clone DRNBAF06 5',
mRNA sequence.


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/tissue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4460 GGACTTTTTTTTTTTTTTTTTTTT 4487
||| ||||| ||||| ||||| ||||| |||||
Db 1 GGT|TTTTTTTTTTTTTTTTTTTTTTT 24

RESULT 278
CF320862
LOCUS      24 bp mRNA linear EST 15-AUG-2003
DEFINITION HD-11-O12.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD-11-O12, mRNA sequence.
ACCESSION  CF320862
VERSION     CF320862.1 GI:33692623
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
1..24
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
    /clone="HD-11-O12"
    /tissue_type="callus"
    /dev_stage="proliferated callus on 2N6 media for 2 weeks"
    /lab_host="E.coli DH10B"
    /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
    /note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT|TTTTTTTTTTTTTTTTTTGCT 4487
||| ||||| ||||| ||||| ||||| |||||
Db 1 TTTT|TTTTTTTTTTTTTTTTTTT 24

RESULT 279
CF320862
LOCUS      24 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0052M17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0052M17 R, genomic survey sequence.
ACCESSION  AZ328848
VERSION     AZ328848.1 GI:10388979
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., fingeay,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: M column: 17
Seq primer: CACACAGAAACACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0052M17"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT|TTTTTTTTTTTTTTTTTTGCT 4487
||| ||||| ||||| ||||| ||||| |||||
Db 24 TTTT|TTTTTTTTTTTTTTTTTTT 1

RESULT 280
AZ363562/c

```

IM0145D02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0145D02 R, genomic survey sequence.
 accession: A2386491.1
 version: A2386491.1
 keywords: GI:10500191
 source: Mus musculus (house mouse)
 organism: Mus musculus
 reference: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 authors: 1 (bases 1 to 24)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 title: Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 journal: Unpublished (2000)
 comment: Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 tel: 801 585 5606
 fax: 801 585 7177
 email: ddunn@genetics.utah.edu
 insert length: 10000
 std error: 0.00
 plate: 0145
 row: D
 column: 02
 seq primer: CACACAGGAACAGCTATGACC
 class: plasmid ends
 high quality sequence stop: 24.
 features: Location/Qualifiers
 source: 1..24

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Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0145D02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PM042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match          0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464  TTTTTCCTTTTTTTTTTTTGCT 4487
Db       24  TTTTTCCTTTTTTTTTTTT    1

```

[illegible]

```

clone UUGC1M0152H07 F, genomic survey sequence.
AZ390642
AZ390642.1 GI:10505685
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: H column: 07
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0152H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTGCT 4487
|||
Db 1 TTTTTTTTTTTTTTTTTTTT 24


RESULT 283
AZ459280
LOCUS
DEFINITION
1M0264A05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUGC1M0264A05 F, genomic survey sequence.
Accession AZ459280
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: H column: 07
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTGCT 4487
|||
Db 1 TTTTTTTTTTTTTTTTTTTT 24


RESULT 284
AZ644621
LOCUS
DEFINITION
IM0508F12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0508F12 R, genomic survey sequence.
Accession AZ644621
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: A column: 05
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTGCT 4487
|||
Db 1 TTTTTTTTTTTTTTTTTTTT 24


RESULT 285
AZ644621
LOCUS
DEFINITION
IM0508F12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0508F12 R, genomic survey sequence.
Accession AZ644621
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0264 row: A column: 05
Seq primer: CGTTGTAAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0264A05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTGCT 4487
|||
Db 1 TTTTTTTTTTTTTTTTTTTT 24


RESULT 286
AZ644621
LOCUS
DEFINITION
IM0508F12R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0508F12 R, genomic survey sequence.
Accession AZ644621
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 20
```


SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Isiam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0243 row: J column: 02 Seq primer: CGTGTGTAACAGCGCCAGT Class: plasmid ends High quality sequence stop: 24.
FEATURES	Location/Qualifiers 1..24 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0243J02" /sex="Female" /lab_host="E. coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC2M library" /note="vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi 4732114.gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
source	Query Match 0.3%; Score 20.8; DB 1; Length 24; Best Local Similarity 91.7%; Pred No. 2e+02; Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	4464 TTTTTTTTTTTTTTTTTTTTTTGCT 4487
Db	24 TTTTTTTTTTTTTTTTTTTTTTTTTT 1
RESULT 287	AZ984490/c
LOCUS	AZ984490
DEFINITION	2M0266H05F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0266H05 F, genomic survey sequence.
ACCESSION	AZ984490
VERSION	AZ984490.1 GI:13855717
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)

RESULT 296	ACCESSION
AZ381039/c	VERSION
LOCUS	KEYWORDS
DEFINITION	

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnhm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

source

1..32
/organism="Oryza sativa"
/mol_type="mrna"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="J30DGS--06-G09"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"

Query Match 0.3%; Score 20.8; DB 1; Length 32;
Best Local Similarity 78.1%; Pred. No. 4e+02;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4020 AAAAAAGACGAAACAATCTTTATTTTTTAT 4051
||||| | |||| | |||| | |||| |
Db 32 AAAAAAAAAAAAAAAAAAATTTTTTTTTTTT 1

RESULT 313

AZ345558

LOCUS CG707472 32 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0080G16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080G16 F, genomic survey sequence.

ACCESSION AZ345558

VERSION AZ345558.1 GI:10424795

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

AUTHORS Unpublished (2000)

JOURNAL Contact: Robert B. Weiss

COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 16
Seq primer: CGTGTGAACAGCGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers

FEATURES source

1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080G16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource


```

/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

Query Match      0.3%; Score 20.6; DB 1; Length 29;
Best Local Similarity 85.2%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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```

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTGCTCTGA 4490
      1 TTTTCTTTTCTTTTCTTTTCTTTGGAAGTGA 27

```

```

RESULT 318
BX553986
LOCUS      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse131902_plc, mRNA sequence.
ACCESSION  BX553986
VERSION     BX553986
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
            Glossina morsitans morsitans
            Glossina morsitans morsitans

```

```

            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes

```

```

JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PubMed     14519198
COMMENT    Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW

```

```

All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES             Location/Qualifiers
     source           1..30
     mol_type="mRNA"
     sub_species="morsitans"
     db_xref="taxon:37546"
     clone="Tse131902_plc"
     tissue_type="adult infected gut"
     clone_lib="Glossina morsitans morsitans adult infected
     gut"
     note="country: Zimbabwe; EST from adult gut infected with
     T.brucei"

```

```

Query Match      0.3%; Score 20.6; DB 1; Length 30;
Best Local Similarity 85.2%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTTTGT 4485
      1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTGT 30
      4 TAGATAGTTTTTTTCTTTTCTTTTCTTTTGT 30

```

```

RESULT 319
BX554615
LOCUS      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse16d08_plc, mRNA sequence.
ACCESSION  BX554615
VERSION     BX554615
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
            Glossina morsitans morsitans
            Glossina morsitans morsitans

```

```

            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 31)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes

```

```

JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PubMed     14519198
COMMENT    Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW

```

```

All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES             Location/Qualifiers
     source           1..30
     mol_type="mRNA"
     sub_species="morsitans"
     db_xref="taxon:37546"
     clone="Tse131902_plc"
     tissue_type="adult infected gut"
     clone_lib="Glossina morsitans morsitans adult infected
     gut"
     note="country: Zimbabwe; EST from adult gut infected with
     T.brucei"

```

```

BX554037
LOCUS      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse13a07_plc, mRNA sequence.
ACCESSION  BX554037
VERSION     BX554037
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
            Glossina morsitans morsitans
            Glossina morsitans morsitans

```

```

            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes

```

```

JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PubMed     14519198
COMMENT    Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW

```

```

All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES             Location/Qualifiers
     source           1..30
     mol_type="mRNA"
     sub_species="morsitans"
     db_xref="taxon:37546"
     clone="Tse13a07_plc"
     tissue_type="adult infected gut"
     clone_lib="Glossina morsitans morsitans adult infected
     gut"
     note="country: Zimbabwe; EST from adult gut infected with
     T.brucei"

```

```

Query Match      0.3%; Score 20.6; DB 1; Length 30;
Best Local Similarity 85.2%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTTTGT 4485
      1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTGT 30
      4 TAGATAGTTTTTTTCTTTTCTTTTCTTTTGT 30

```

```

RESULT 320
BX554615
LOCUS      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse16d08_plc, mRNA sequence.
ACCESSION  BX554615
VERSION     BX554615
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
            Glossina morsitans morsitans
            Glossina morsitans morsitans

```

```

            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 31)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes

```

```

JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PubMed     14519198
COMMENT    Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW

```

```

All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES             Location/Qualifiers
     source           1..30
     mol_type="mRNA"
     sub_species="morsitans"
     db_xref="taxon:37546"
     clone="Tse13a07_plc"
     tissue_type="adult infected gut"
     clone_lib="Glossina morsitans morsitans adult infected
     gut"
     note="country: Zimbabwe; EST from adult gut infected with
     T.brucei"

```

```

Query Match      0.3%; Score 20.6; DB 1; Length 30;
Best Local Similarity 85.2%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTTTGT 4485
      1 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTGT 30
      4 TAGATAGTTTTTTTCTTTTCTTTTCTTTTGT 30

```

```

RESULT 320
BX554615
LOCUS      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse16d08_plc, mRNA sequence.
ACCESSION  BX554615
VERSION     BX554615
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
            Glossina morsitans morsitans
            Glossina morsitans morsitans

```

```

            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 31)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes

```

JOURNAL
MEDLINE
PUBMED
COMMENT

response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source

1..31
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse26a12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 20.6; DB 1; Length 31;
Best Local Similarity 85.2%; Pred. No. 4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTGT 4485
DB 4 TAGATAGTTTTTTTTTTTTTTTTTTGT 30

RESULT 321
LOCUS BX556269 31 bp mRNA linear EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse26a12_plc, mRNA sequence.
ACCESSION BX556269
VERSION BX556269.1 GI:33380198
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 31)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
Location/Qualifiers

1..31
source
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse26a12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 20.6; DB 1; Length 31;
Best Local Similarity 85.2%; Pred. No. 4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTGT 4485
DB 4 TAGATAGTTTTTTTTTTTTTTTTTTGT 30

RESULT 322
LOCUS AW332181 22 bp mRNA linear EST 31-JAN-2000
DEFINITION S5C7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW332181
VERSION AW332181.1 GI:6828538
KEYWORDS EST.
SOURCE Pneumocystis carinii
ORGANISM Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae; Pneumocystis.
REFERENCE 1 (bases 1 to 22)
AUTHORS Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C., Edman, J.C., Kovacs, J. and Cushion, M.
TITLE Expressed sequence tags from Pneumocystis carinii
JOURNAL Unpublished (2000)
COMMENT School of Biological Sciences
University of Kentucky
101 Morgan Building, University of Kentucky, Lexington, KY 40506-0255, USA
Tel: 606 257 2161
Fax: 606 257 1717
Email: staben@pop.uky.edu.

FEATURES
source
1..22
Location/Qualifiers
/organism="Pneumocystis carinii"
/mol_type="mRNA"
/db_xref="taxon:4754"
/lab_host="E. coli"
/clone_lib="AGS-1"
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat (99-1-6, sacrificed on 3/17/99) at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTGT 4485
DB 1 TTTTTTTTTTTTTTTTTTTT 22

RESULT 323
LOCUS AW332399 22 bp mRNA linear EST 31-JAN-2000
DEFINITION SBA2 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW332399


```

ACCESSION      AZ351527
VERSION        AZ351527.1   GI:10430764
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., . Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert length: 10000    Std Error: 0.00
                Plate: 0089 row: E column: 07
                Seq primer: CACACAGGAACAACGCTATGACC
                Class: plasmid ends
                High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     1..22            /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGCI0M0089E07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGCIM library"
                     /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464  TTTTTCCTTTTTTTTTTTTTTTGT 4485
Db       22  TTTTTCCTTTTTTTTTTTTTTTT 1

RESULT 338
AZ357630/C
LOCUS      AZ357630
DEFINITION IM0099M15F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0099M15 F, genomic survey sequence.
ACCESSION  AZ357630

```

KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Iglam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0127 row: H column: 16
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
Location/Qualifiers
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/db_xref="taxon:10090"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 22 TTTTTCCTTTTTCCTTTTTCCTTC 1

RESULT 340
AZ388103/c
LOCUS AZ388103
DEFINITION M0147N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0147N14 R, genomic survey sequence.
ACCESSION AZ388103
VERSION AZ388103.1 GI:10501811
KEYWORDS GSS.

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: gdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CCGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 22.

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1. 22
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/mol_type="genomic DNA"
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/db_xref="taxon:10090"
/clone="UUGC1M055424"
/sex="Male"

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUG1M library"
/note="vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrotomically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt-end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```
Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 4464 TTTTTTTTTTTTTTTTTTGT 4485
D6 22 TTTTTTTTTTTTTTTTTT 1

RESULT	351
AZ779844	
LOCUS	AZ779844
DEFINITION	22 bp DNA linear GSS 16-FEB-2001 2M0016112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0016112 R, genomic survey sequence.

ACCESSION	AZ779844	GI:12910910
VERSION	AZ779844.1	

Mus musculus (house mouse)

Musculus

Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata;
Mammalia; Rutheria;
1 (bases 1 to 22)

MEENEN, E., LONGACRE, S., MAHMOUD, M., MEENEN, E., PEDERSEN, T., REILLY, M., ROSE, R., ROSE, R., STOKES, R., TINGEY, A., VON NIEDERHAUSEN, A. and WRIGHT, D., WEISS, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

RESULT 363
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FEATURES

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Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (Gill4732114[gblAF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
pb 23 TTTTTTTTTTTTTTTTTTTTTT 2

LOCUS	AZ419236	23 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	M019SH07R Mouse 10kb plasmid UGCI1M library Mus musculus genomic clone UGCI1M019SH07 R, genomic survey sequence.				

VERSION AZ419236.1 GI:10543249

SOURCE Mus musculus (house mouse)

REFERENCE
1 (bases 1 to 23)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

ADAMS
Dunn, D., Aoyagi, R., Barber, M., Beacoin, J., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

CONTACT: ROBERT D. MEIER
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0195 row: H column: 07
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	1. Open-Source Datasets: The model is trained on a large, diverse dataset of open-source data, ensuring it can handle a wide range of inputs.
2. Scalability: The model is designed to scale efficiently, allowing it to process large volumes of data without significant performance degradation.	2. Community Feedback: The model's performance is continuously improved through feedback from the open-source community, ensuring it remains up-to-date and effective.
3. Interpretability: The model's internal logic is transparent, making it easy to understand and debug, which is crucial for applications requiring high transparency.	3. Regular Updates: The model is updated regularly with the latest research and data, ensuring it stays at the forefront of its field.
4. Flexibility: The model can be adapted to various tasks and environments, making it a versatile tool for many different applications.	4. Documentation: Comprehensive documentation is provided for the model, making it easy for users to get started and troubleshoot any issues.
5. Performance: The model demonstrates superior performance compared to other models in its class, particularly in terms of speed and accuracy.	5. Integration: The model is designed to integrate seamlessly with existing systems and workflows, making it a practical choice for many users.

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="JUGClM0195H07"
/sex="Male"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnates/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi47321134.gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels

QY 4464 TTTTITTTTTTTTTTTTGT 4485
Db 1 TTTTITTTTTTTTTTTTTTTT 22

RESULT 380
AZ461220/C

LOCUS	23 bp	DNA	linear	GSS 04-OCT-2000
AZ461220	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0267D05	F ₂	genomic survey	sequence.

ACCESSION AZ461220
 VERSION AZ461220.1 GI:10619345
 KEYWORDS GSS.

SOURCE *MUS MUSCULUS* (HOUSE MOUSE)
MUS MUSCULUS

ORGANISM

REFERENCE 1 (bases 1 to 23)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhauzen, A. and Wright, D. Weizen D.

TITLE Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
Unpublished (2000)
plasmid inserts

JOURNAL COMMENT
unpublished (2000)
Contact: Robert B. Weiss

CONTACT: ROBERT B. WEISS
University of Utah Genome Center

University of Utah
University of Utah
Rm. 308, Biomedical
Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
Tel: 801 585 5506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Seq: 0267 row: D column: 05
Seq primer: CGTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

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musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gil4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels

Qy 4464 TTTTITTTTTTTTTTTTGT 4485
pB 23 TTTTITTTTTTTTTTTTTTTT 2

RESULT 381

Accession	AF046532	Accession	AF046532
LOCUS	LOCUS	LOCUS	LOCUS
DEFINITION	DEFINITION	DEFINITION	DEFINITION
Mouse 10kb plasmid UGCG1M library	Mouse 10kb plasmid UGCG1M library	Mouse 10kb plasmid UGCG1M library	Mouse 10kb plasmid UGCG1M library
clone UGCG1M0275K12 F. genomic survey sequence.	clone UGCG1M0275K12 F. genomic survey sequence.	clone UGCG1M0275K12 F. genomic survey sequence.	clone UGCG1M0275K12 F. genomic survey sequence.
23 bp DNA	23 bp DNA	23 bp DNA	23 bp DNA
linear	linear	linear	linear
GSS 04-OCT-2000	GSS 04-OCT-2000	GSS 04-OCT-2000	GSS 04-OCT-2000

ACCESSION
AZ465327

VERSION AZ465327.1 GI:10623452

KEYWORDS GSS.

SOURCE *Mus musculus* (house mouse)

ORGANISM	Mus musculus
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100	

Eukaryota; Metazoa; Chorda

Mammalia; Eutheria; Rodentia

REFERENCE 1 (bases 1 to 23)

AUTHORS
Dunn, D., Aoyagi, A., Barber
Tolan, P., Longacre, S., Mah

Islam, H., Longacre, S., Mah-

Reilly, M., Rose, M., Rose, K., Niederhansen A. and Wrich

TITLE Mause whole genome scaffold
Niederhausern, A. and Wright

TITLE
Mouse whole genome scaffold
plasmid inserts

plasmid inserts
published (2000)

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss

CONTACT: ROBERT B. WEISS
University of Utah Genome

University of Utah
University of Utah Genome Institute

University of Otago
Rm. 308, Biomedical Polymer

AM: 306, Biomedical Research
84112, USA

plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical
Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Plate: 0455 row: J column: 07

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Class: plasmid ends
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTTTTTTTGTTGT 4485
Db 1 TTTTTCCTTTTTTTTTTTT 22

RESULT 388
AZ654903/c
LOCUS
DEFINITION
23 bp DNA linear GSS 14-DEC-2000
1M0529D03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0529D03 R, genomic survey sequence.
ACCESSION
AZ654903
VERSION
AZ654903.1 GI:11792049
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0529 row: D column: 03
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends

FEATURES
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High quality sequence stop: 23.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0514E09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTTTTTTTGTTGT 4485
Db 1 TTTTTCCTTTTTTTTTTT 22

RESULT 388
AZ654903/c
LOCUS
DEFINITION
23 bp DNA linear GSS 16-FEB-2001
2M0014008F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0014008 F, genomic survey sequence.
ACCESSION
AZ778751
VERSION
AZ778751.1 GI:12908711
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: O column: 08
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

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source

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Location/Qualifiers
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/clone="UUGC2M0014008"
/sex="Male"
/lab_host="E. Coli strain Xl10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/nucleic_acid="pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match	0.3%	Score 20.4;	DB 1;	Length 23;
Best Local Similarity	95.5%	Pred. No. 2.2e+02;		
Matches 21;	Conservative	0;	Mismatches 1;	Indels 0;
Matches 0;	Gap	0;	Gap	0;

	4464	TTTTTTTTTTTTTTTTTTGT	4485
Qy			
D _b	23	TTTTTTTTTTTTTTTTTTTT	2

RESULT 390	AZ787184	23 bp	DNA	linear	GSS 16-FEB-2001
AZ787184/c	2M0033C07F	Musae 10kb	plasmid	UGCCIM library	Mus musculus genomic
LOCUS	clone UGCC2M0033C07 F,	genomic survey	sequence.		
DEFINITION	AZ787184	1 GI:12925692			
ACCESSION	AZ787184				
VERSION	AZ787184				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1. (bases 1 to 23)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.				
TITLE	Musae whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0033 row: C column: 07 Seq primer: CGTTGTAACGACGCCAGT Class: plasmid ends High quality sequence stop: 23. Location/Qualifiers				
FEATURES					

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0059J16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G1[4732114]gb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match 0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred.No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTITTTTTTTTTTTTTTTGT 4485
DB 22 TTTTITTTTTTTTTTTTAT 1

RESULT 393
AZ817623/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ817623 23 bp DNA linear GSS 20-FEB-2001
2M0087N09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0087N09 F, genomic survey sequence.
AZ817623
GSS.
AZ817623.1 GI:12987531
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: drunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0087 row: N column: 09
Seq primer: CGTTGTAAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
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/mol_type="genomic DNA"

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/strain="C57BL/6J"
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/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483
DB 22 AATTTTTTTTTTTTTTTTTT 1

RESULT 394
A2859570/c
LOCUS
DEFINITION
2M0165B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0165B14 F, genomic survey sequence.
ACCESSION
A2859570
VERSION
A2859570.1 GI:13054022
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: B column: 14
Seq primer: CTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
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/mol_type="genomic DNA"
/strain="C57BL/6J"

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0087N09"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483
DB 22 AATTTTTTTTTTTTTTTTTT 1

RESULT 395
A2939608/c
LOCUS
DEFINITION
2M0198I07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0198I07 R, genomic survey sequence.
ACCESSION
A2939608
VERSION
A2939608.1 GI:13800390
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0198 row: I column: 07
Seq primer: CACACAGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/db_xref="taxon:10090"
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/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTT 4485
DB 23 TTTTTTTTTTTTTTTTTT 2

RESULT 395
A2939608/c
LOCUS
DEFINITION
2M0198I07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0198I07 R, genomic survey sequence.
ACCESSION
A2939608
VERSION
A2939608.1 GI:13800390
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0198 row: I column: 07
Seq primer: CACACAGAAACACGTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
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/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC2M0198107"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
Db      23 TTTTTTTTTTTTTTTTTTTT 2

RESULT 396
BH000534
LOCUS      23 bp      DNA      linear      GSS 27-APR-2001
DEFINITION      2M0288B03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0288B03 R, genomic survey sequence.
ACCESSION      BH000534
VERSION      BH000534.1 GI:13871760
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 23)
AUTHORS      Dunn,D., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Islam,H., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 Row: B Column: 03
Seq primer: CACACAGGAACACACTATGACC
Class: plasmid ends
High quality sequence stop: 23.
FEATURES      Location/Qualifiers
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0288B03"

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/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
Db      1 TTTTTTTTTTTTTTTTTTTT 22

RESULT 397
TA151C02Q/c
LOCUS      23 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION      T. brucei sheared genomic DNA clone 151c02, reverse sequence,
genomic survey sequence.
ACCESSION      AL473028
VERSION      AL473028.1 GI:11838301
KEYWORDS      GSS.
SOURCE      Trypanosoma brucei
ORGANISM      Trypanosoma brucei
REFERENCE      1 (bases 1 to 23)
AUTHORS      Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL      Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
rhl@sanger.ac.uk
COMMENT      Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: rnelayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES      Location/Qualifiers
source      1..23
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Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTTTTTGT 4485
Db 23 TTTT...TTTTTTTTTTT 2

RESULT 398
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LOCUS TA274B03P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 274B03, forward sequence,
genomic survey sequence.
ACCESSION AL484584
VERSION AL484584.1 GI:11851281
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
LOCATION/QUALIFIERS
source 1. .23
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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTTTTTGT 4485
Db 23 TTTT...TTTTTTTTTTT 2

RESULT 399
TA353A10P/c
LOCUS TA353A10P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
LOCATION/QUALIFIERS
source 1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTTTTTGT 4485
Db 1 TTTT...TTTTTTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
LOCATION/QUALIFIERS
source 1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTTTTTGT 4485
Db 1 TTTT...TTTTTTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
LOCATION/QUALIFIERS
source 1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTTTTTGT 4485
Db 1 TTTT...TTTTTTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
LOCATION/QUALIFIERS
source 1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTTTTTGT 4485
Db 1 TTTT...TTTTTTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/t_brucei/.
LOCATION/QUALIFIERS
source 1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274B03"

Query Match      0.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 26)
AUTHORS Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1384
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 1384 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 1.
FEATURES
source
1..26
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538233"
/db_xref="taxon:9606"
/clone="IMAGE:132611"
/sex="Female"
/dev_stages="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2Hp"
/name="Organ: placenta; Vector: pVT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AACTGAGAAATTCGCGCCGAGAAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. "
Query Match 0.3%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTGT 4485
DB 1 TTTTCTTTTCTTTTCTTTTCTT 22

RESULT 404
CNS00BGV 26 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR23F05 of RPCL-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL057060 GI:4937627
VERSION AL057060
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 26)
AUTHORS Genoscope.

```

```

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCL-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1..26
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR23F05"
/clone_lib="RPCL-98"
/note="end : TET3"
FEATURES
source
1..26
Query Match 0.3%; Score 20.4; DB 1; Length 26;
Best Local Similarity 87.5%; Pred. No. 2.9e+02;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTTCTTGT 4486
DB 1 CTTTCTTTTCTTTTCTTTTCTT 24

RESULT 405
TA321G11P/c 26 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 321g11, forward sequence,
DEFINITION Genomic survey sequence.
ACCESSION AL492371
VERSION AL492371.1 GI:11867375
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 26)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsaved@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..26
/organism="Trypanosoma brucei"
FEATURES
source

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QY	4464	TTTTTTTTTTTTTTTTTTTTTGT 4485
Db	1	TTTTTTTTTTTTTTTTTTTTT 22
RESULT 407		
TS2979		
LOCUS		
DEFINITION		
ACCESSION	TS2979	27 bp mRNA linear EST 06-FEB-1995
VERSION	Ya82e08.s1	Stratagene ovary (#937217) Homo sapiens cDNA clone
KEYWORDS	IMAGE:68198	3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN
SOURCE	PRECURSOR (HUMAN)	, mRNA sequence.
ORGANISM	TS2979.1	GI:654839
	EST.	
	Homo sapiens (human)	
REFERENCE		
AUTHORS		
	1	(bases 1 to 27)
	1	Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
	1	Chisaoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
	1	Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
	1	Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
	1	Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
	1	Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
	1	and Marra,M.
TITLE		Generation and analysis of 280,000 human expressed sequence tags
JOURNAL		Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478	
PUBMED	8889549	
COMMENT		
	Other ESTs: ya82e08.x1	
	Contact: Wilson RK	
	Washington University School of Medicine	
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
	Tel: 314 286 1800	
	Fax: 314 286 1810	
	Email: est@wustl.wustl.edu	
	Insert Size: 577	
	High quality sequence starts: 1	High quality sequence stops: 1
	Source: IMAGE Consortium, LLNL This clone is available royalty-free	
	through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov)	
	for further information. Trace considered overall poor quality	
	Insert length: 577	Std Error: 0.00
	Seq primer: -21m13	
FEATURES		
source		
	1..27	Location/Qualifiers
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	/mol_type="mRNA"	
	/db_xref="GDB:504455"	
	/db_xref="taxon:9606"	
	/clone="IMAGE:68198"	
	/sex="female"	
	/dev_stage="49 year old"	
	/lab_host="SOLR cells (kanamycin resistant)"	
	/clone_lib="Stratagene ovary (#937217)"	
	/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;	
	Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt.	
	Total ovary tissue, normal, caucasian. Average insert	
	size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5'	
	GAAATCGGCACGAG 3' ~3' adaptor sequence: 5'	
	CTCGAGTTTTTTTTTTTTTTT 3"	
Query Match	0.3%	Score 20.4; DB 1; Length 27;
Best Local Similarity	91.3%	Pred. No. 3.2e+02;
Matches 21; Conservative	0; Mismatches 2;	Indels 0; Gaps 0;
QY	4464	TTTTTTTTTTTTTTTTTTTGT 4486
Db	3	TTTTTTTTTTTTTTTTTTGCC 25
RESULT 408		

LOCUS	28 bp	DNA	linear	GSS 02-OCT-2000
DEFINITION	clone0991115F Mouse 10kb plasmid UGCM library Mus musculus genomic			
ACCESSION	AZ357605.1			
VERSION	AZ357605.1			
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 28) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0099 row: 1 column: 15 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 28. Location/Qualifiers			
FEATURES				

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Location/Qualifiers
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0099115"
/sex="Male"
/lab_host="E. Coli strain XU10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb Plasmid UUGC1M library"
/note="Vector: PWB42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XU10-Gold (Stratagene) cells and selected for ampicillin resistance."
FEATURES

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Query Match      0.3%; Score 20.4; DB 1; Length 28;
Best Local Similarity 95.5%; Pred.No. 3.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 4462 ACTTTTITTTTTTTTTTTTTTTT 4483
| | | | | | | | | | | | | |
Db 22 AATTTTTTTTTTTTTTTTTTTT 1

RESULT 410	29 bp	mpna	linear	EST 04-SEP-2003
AL048747/C				
LOCUS	AL048747			

DEFINITION DKFZp566K043_r1 566 (synonym: hFkd2) Homo sapiens cDNA clone
ACCESSION DKFZp566K043, mRNA sequence.
VERSION AL048747
KEYWORDS AL048747.1 GI:4727818
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE ESR (koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
location/Qualifiers
1..29
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566K043"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hFkd2)"
/note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.3; Score 20.4; DB 1; Length 29;
Best Local Similarity 95.5; Pred.No.3.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4465 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 29 TTTTTCCTTTTTCCTTTTTCCTTC 8
|||||

RESULT 411
BQ586486/c
LOCUS BQ586486 29 bp mRNA linear EST 06-DEC-2002
DEFINITION E012391-024-012-J22-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-012-J22 5-PRIME, mRNA sequence.
ACCESSION BQ586486
VERSION BQ586486.1 GI:26116068
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 29)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruock,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 29 Std Error: 0.00
Plate: 12 row: J column: 22
Seq primer: SP6; CATACGATTGATGACACTATAG.
Location/Qualifiers
1..29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding


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FEATURES
source
  High quality sequence stop: 29.
  Location/Qualifiers
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      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC2M0100N08"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 29;
Best Local Similarity 95.5%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTT 4483
Db 23 ATTTTTTTTTTTTTTTTTTT 2

RESULT 416
TA378G07P
LOCUS      29 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 378g07, forward sequence, genomic survey sequence.
ACCESSION  AL497621
VERSION     AL497621.1  GI:11873343
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
ORGANISM    Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
            Email: nelsaved@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
  Query Match      0.3%; Score 20.4; DB 1; Length 29;
  Best Local Similarity 95.5%; Pred. No. 3.7e+02;
  Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTT 4485
Db 1 TTTTTTTTTTTTTTTTTTTT 22

RESULT 417
BE539470
LOCUS      30 bp      mRNA      linear      EST 09-AUG-2000
DEFINITION 601060134F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446720 5', mRNA sequence.
ACCESSION  BE539470
VERSION     BE539470.1  GI:9768115
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 30)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Incyte Genomics, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Plate: LLAM8419 row: c column: 09
            High quality sequence stop: 30.
            Location/Qualifiers
              1..30
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3446720"
                /cell_line="MGC36"
                /lab_host="DH10B"
                /clone_lib="NIH MGC 10"
                /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5 kb. Library prepared by Life Technologies."

Query Match      0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 52 GCGCGCAACGAGGCTGCGGGCGCGCGGC 81
Db 1 GGCAGCTACGCGGGCGCGCGCGTGGCGC 30

RESULT 418
BM280395
LOCUS      30 bp      mRNA      linear      EST 17-SBP-2002
DEFINITION 3'EST-NCID15-143 human CD15+ myeloid progenitor cells cDNA library Homo sapiens cDNA 3', mRNA sequence.
ACCESSION  BM280395

```

```

VERSION BM280395.1 GI:23025929
SOURCE EST.
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Chen, J., Sun, M., Lee, S., Zhou, G., Rowley, J. D. and Wang, S. M.
TITLE Identifying novel transcripts and novel genes in the human genome
        by using novel SAGE tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (19), 12257-12262 (2002)
COMMENT Contact: Wang SM
        Hem/Onc
        University of Chicago Medical Center
        5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
        Tel: 773-702-6788
        Fax: 773-702-3002
        Email: swangl@midway.uchicago.edu
This EST fragment was amplified from human CD15+ myeloid progenitor
cells cDNA library with GLGI technique (Generation of Longer cDNA
fragments from SAGE tags for Gene Identification, Proc. Natl. Acad.
Sci. USA 97, 349, 2000). A high-throughput GLGI procedure for
converting a large number of SAGE tag sequences into 3' ESTs,
Genes, Chromosomes & Cancers, in press), which starts from the 3'
end till the last CATG site of the target cDNA sequence.
Seq primer: M13 Forward.

FEATURES
        source
        Location/Qualifiers
            1..30
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="bone marrow"
            /cell_type="CD15+ myeloid progenitor cells"
            /clone_lib="human CD15+ myeloid progenitor cells cDNA
            Library"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTCTTCTGACATG 4496
      |||||
Db 1 TTTTCTTTTCTTCTGACATG 30

RESULT 419
BX549675 30 bp mRNA linear EST 10-OCT-2003
LOCUS
DEFINITION BX549675 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse109c08_pic, mRNA sequence.
ACCESSION BX549675
VERSION
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 30)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
        Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
        morsitans morsitans and expression analysis of putative immune
        response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
        Pathogen Sequencing Unit
        The Sanger Institute The Wellcome Trust Genome Campus
        Hinxton, Cambridge, CB10 1SA, UK
        Request for clones, please contact: Mike Lehane
        Prof. M.J. Lehane
        School of Biological Sciences,
        University of Wales,
        Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
        source
        Location/Qualifiers
            1..30
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /db_xref="taxon:37546"
            /clone="Tse109c08_pic"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTT 4483
      |||||
Db 9 AGTTTCTTTTCTTTTCTTTT 30

RESULT 420
BX551003
LOCUS
DEFINITION BX551003 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse116a06_pic, mRNA sequence.
ACCESSION BX551003
VERSION
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 30)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
        Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
        morsitans morsitans and expression analysis of putative immune
        response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
        Pathogen Sequencing Unit
        The Sanger Institute The Wellcome Trust Genome Campus
        Hinxton, Cambridge, CB10 1SA, UK
        Request for clones, please contact: Mike Lehane
        Prof. M.J. Lehane
        School of Biological Sciences,
        University of Wales,
        Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
        source
        Location/Qualifiers
            1..30
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /db_xref="taxon:37546"
            /clone="Tse116a06_pic"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"

```


Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1. .30
Location/Qualifiers

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse43e07_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTTTT 4483

Db 9 AGTTTTTTTTTTTTTTTTTTT 30

RESULT 424

LOCUS BX563547 30 bp mRNA linear EST 10-OCT-2003
DEFINITION BX563547 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse67e03_plc, mRNA sequence.

ACCESSION BX563547
VERSION BX563547.1 GI:33430769

KEYWORDS EST.
SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 30)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1. .30
Location/Qualifiers

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"

/clone="Tse67e03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTTTT 4483

Db 9 AGTTTTTTTTTTTTTTTTTTT 30

RESULT 425

LOCUS BX565972 30 bp mRNA linear EST 14-OCT-2003
DEFINITION BX565972 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse7e12_plc, mRNA sequence.

ACCESSION BX565972
VERSION BX565972.1 GI:33433017

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 30)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1. .30
Location/Qualifiers

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"

/clone="Tse7e12_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTTTT 4483

Db 9 AGTTTTTTTTTTTTTTTTTTT 30

RESULT 426


```

SOURCE      Mus musculus (house mouse)
ORGANISM
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0094 row: D column: 14
             Seq primer: CACACAGGAACACGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 26.
FEATURES     Location/Qualifiers
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             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC1M0094D14"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /notes="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
             Query Match      0.3%; Score 20.2; DB 1; Length 26;
             Best Local Similarity 88.0%; Pred. No. 3.1e+02;
             Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 26 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 437
AZ623156
LOCUS      26 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0460L01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0460L01 R, genomic survey sequence.
ACCESSION  AZ623156
VERSION     AZ623156.1 GI:11745346
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
             plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0460 row: L column: 01
             Seq primer: CACACAGGAACACGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 26.
FEATURES     Location/Qualifiers
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             /organism="Mus musculus"
             /mol_type="genomic DNA"
             /strain="C57BL/6J"
             /db_xref="taxon:10090"
             /clone="UUGC1M0460L01"
             /sex="Male"
             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
             /clone_lib="Mouse 10kb plasmid UUGC1M library"
             /notes="Vector: PWD42nv; Purified genomic DNA from M.
             musculus C57BL/6J (male) was obtained from the Jackson
             Laboratory Mouse DNA Resource
             (http://www.jax.org/resources/documents/dnares/). The DNA
             was hydrodynamically sheared by repeated passage through a
             0.005 inch orifice at constant velocity. The sheared DNA
             was blunt end-repaired with T4 DNA polymerase and T4
             polynucleotide kinase. Adaptor oligonucleotides were
             ligated to the blunt ends in high molar excess. The
             adaptor DNA was purified and size-selected for a 9.5 to
             10.5 kb range using preparative agarose gel
             electrophoresis. Vector DNA was prepared from a derivative
             of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
             inducible derivative of plasmid R1. The vector was ligated
             with adaptors complementary to the insert adaptors and
             purified. The sheared, adaptor mouse DNA was annealed to
             adaptor vector DNA, and transformed into
             chemically-competent E. coli XL10-Gold (Stratagene) cells
             and selected for ampicillin resistance."
             Query Match      0.3%; Score 20.2; DB 1; Length 26;
             Best Local Similarity 88.0%; Pred. No. 3.1e+02;
             Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 438
AZ635695
LOCUS      26 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0493G18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0493G18 F, genomic survey sequence.
ACCESSION  AZ635695
VERSION     AZ635695.1 GI:11757885
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0493 row: G column: 18
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 26.
FEATURES
source
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0493G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.3%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 3.1e-02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTTCCTTTTTCCTTTTCTCTT 4488
Db 1 TTTTTCCTTTTTCCTTTTCTCTT 25

RESULT 439
CF298133 27 bp mRNA linear EST 15-AUG-2003
LOCUS
7LEAF--01-G09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-G09, mRNA sequence.
ACCESSION
CF298133
VERSION
CF298133.1 GI:33669894
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Mahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-G09"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 20.2; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTTCCTTTTTCCTTTTCTCTT 4488
Db 3 TTTTTCCTTTTTCCTTTTCTCTT 27

RESULT 440
A2434285/c 27 bp DNA linear GSS 03-OCT-2000
LOCUS
1M0220B08R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0220B08 R, genomic survey sequence.
ACCESSION
A2434285
VERSION
A2434285.1 GI:10558298
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0220 row: B column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
FEATURES
source
1..27

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0220B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 20.2; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4464 TTTTTCCTTTTTCCTTTCCTT 4488
      ||||| ||||| ||||| |||||
DB 27 TTTTTCCTTTTTCCTTTCCTT 3

```

```

RESULT 441
AZ458228/c
LOCUS
DEFINITION
  AZ458228 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0262C12 F, genomic survey sequence.
ACCESSION
  AZ458228
VERSION
  AZ458228.1 GI:10616353
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 27)
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausen,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert length: 10000 Std Error: 0.00
  Plate: 0262 row: C column: 12
  Seq primer: CGTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 27.
FEATURES
  source
    1..27
    /organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0262C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.3%; Score 20.2; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 4464 TTTTTCCTTTTTCCTTTCCTT 4488
      ||||| ||||| ||||| |||||
DB 27 TTTTTCCTTTTTCCTTTCCTT 3

```

```

RESULT 442
AL587605
LOCUS
DEFINITION
  AL587605 BP Chicken Brain Library Gallus gallus cdna clone
  ROS059F11, mRNA sequence.
ACCESSION
  AL587605
VERSION
  AL587605.1 GI:13192639
KEYWORDS
  EST.
SOURCE
  Gallus gallus (chicken)
ORGANISM
  Gallus gallus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
  1 (bases 1 to 28)
REFERENCE
  Murray,F.
  BP Chicken Brain Library
  Unpublished (2001)
  Contact: Frazer Murray
  Dept. Genomics and Bioinformatics
  Roslin Institute
  Roslin, Midlothian, EH25 9PS, UK
  Tel: +44 (0)131 527 4200
  Fax: +44 (0)131 440 0434
  Email: frazer.murray@bbsrc.ac.uk
  CGCGCGCTTTTTCCTTTCCTT 3' Poly A RNA purchased from Clontech
  (*6854-
  Seq primer: M13F.
  Location/Qualifiers
    1..28
    /organism="Gallus gallus"
    /mol_type="mRNA"
    /db_xref="taxon:9031"
    /clone="ROS059F11"
    /tissue type="Brain"
    /dev stage="Unknown"
    /lab_host="DH10B"
    /clone_lib="BP Chicken Brain Library"

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Query Match	0.3%	Score 20.2;	DB 1;	Length 29;
Best Local Similarity	88.0%;	Pred. No. 4e+02;		


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DEFINITION AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
sequence.
ACCESSION AU268044
VERSION AU268044.1 GI:20526842
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 31)
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
1..31
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH836"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.3%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
Db 26 TTTTAAATTTTCTTTTCTTTTCTTTTCTTT 2

RESULT 451
BO591372 31 bp mRNA linear EST 06-DEC-2002
LOCUS E012712-024-017-115-T7 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION cDNA clone 024-017-115 3-PRIME, mRNA sequence.
ACCESSION BO591372
VERSION BO591372.1 GI:26120955
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 31)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stalh,D., Wruck,M., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 31 Std Error: 0.00
Plate: 17 row: 1 column: 15
Seq primer: T7; GTAATACGACTCCTATAGGCG.
Location/Qualifiers

FEATURES
source
1..31
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188741"
/db_xref="taxon:161934"
/clone="024-017-115"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 25

RESULT 452
CF297930 31 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--01-B17-g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--01-B17, mRNA sequence.
ACCESSION CF297930
VERSION CF297930.1 GI:33669691
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 31)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..31
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-B17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;

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Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT...TTT 4488
 Db 31 TTTT...TTT 7

RESULT 453
 AZ486763
 LOCUS
 DEFINITION 31 bp DNA linear GSS 05-OCT-2000
 clone UUGC1M0315A11 P, genomic survey sequence.
 ACCESSION AZ486763
 VERSION AZ486763.1 GI:10653856
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weisse, R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE
 JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0315 row: A column: 11
 Seq primer: CTTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 31.

FEATURES
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 1..31
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0315A11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20.2; DB 1; Length 31;
 Best Local Similarity 88.0%; Pred. No. 4.6e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT...TTT 4488
 Db 1 TTTT...TTT 25

RESULT 454
 AZ785111
 LOCUS
 DEFINITION 31 bp DNA linear GSS 16-FEB-2001
 clone UUGC2M0028B14 R, genomic survey sequence.
 ACCESSION AZ785111
 VERSION AZ785111.1 GI:12921525
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE
 JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0028 row: B column: 14
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 31.

FEATURES
 source
 1..31
 Location/Qualifiers

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0028B14"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20.2; DB 1; Length 31;
 Best Local Similarity 88.0%; Pred. No. 4.6e+02;
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;


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Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 458
CF282414/c
LOCUS
DEFINITION 14ETL--09-O19.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION CF282414 20 bp mRNA linear EST 14-AUG-2003
VERSION Oryza sativa cDNA clone 14ETL--09-O19, mRNA sequence.
KEYWORDS EST.
SOURCE CF282414.1 GI:33659801
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-O19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 20

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-O19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

RESULT 460
CF301720
LOCUS
DEFINITION 7LEAF--06-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--06-L01, mRNA sequence.
ACCESSION CF301720
VERSION CF301720.1 GI:33673481
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-L01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 20

FEATURES
source
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--06-L01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

RESULT 459
CF299822
LOCUS
DEFINITION 7LEAF--03-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-P22, mRNA sequence.
ACCESSION CF299822
VERSION CF299822.1 GI:33671583
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs

```

```

Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 4464 TTTT... 4483
Db 1 TTTT... 20

RESULT 461
CF302027 20 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--07-C16.bi Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--07-C16, mRNA sequence.
ACCESSION CF302027
VERSION CF302027.1 GI:33673788
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-C16"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4483
Db 1 TTTT... 20

RESULT 462
CF310604/c 20 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-F14, mRNA sequence.
ACCESSION CF310604
VERSION CF310604.1 GI:33682365
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-F14"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4483
Db 20 TTTT... 1

RESULT 463
CF313067/c 20 bp mRNA linear EST 15-AUG-2003
LOCUS HD--01-B02.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-B02, mRNA sequence.
ACCESSION CF313067
VERSION CF313067.1 GI:33684828
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-B02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-13-B05"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI. Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 467 20 bp mRNA linear EST 18-AUG-2003
 CF328565/c LOCUS
 NACL--03-F14.b1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION
 sativa cDNA clone NACL--03-F14, mRNA sequence.
 ACCESSION
 CF328565
 VERSION
 CF328565.1 GI:33805376
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 Oryza sativa
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)

REFERENCE
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 SOURCE
 location/Qualifiers
 1..20

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 20 TTTT TTTT TTTT TTTT TTTT 1

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RESULT 468 20 bp mRNA linear EST 18-AUG-2003
CF333173 LOCUS
JMT--01-P11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--01-P11, mRNA sequence.
DEFINITION
CF333173
ACCESSION
CF333173.1 GI:33814617
VERSION
CF333173.1
KEYWORDS
EST.

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SOURCE
 ORGANISM
 Oryza sativa

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)

REFERENCE
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 SOURCE
 location/Qualifiers
 1..20

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="JMT--01-P11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis jasmonic acid methyltransferase overexpression line."

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Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 469 20 bp mRNA linear EST 18-AUG-2003
 CF334170 LOCUS
 JMT--03-F17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--03-F17, mRNA sequence.
 DEFINITION
 CF334170
 ACCESSION
 CF334170.1 GI:33816671
 VERSION
 CF334170.1
 KEYWORDS
 EST.

SOURCE
 ORGANISM
 Oryza sativa

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 20)

REFERENCE
 AUTHORS
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 CONTACT: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

COMMENT

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Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source

1. .20
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/clone lib="AcJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 470

CF336525 20 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--06-J21.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--06-J21, mRNA sequence.
CF336525
VERSION CF336525.1 GI:33821425
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1. .20
/organism="Oryza sativa"
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/clone="JMT--06-J21"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="AcJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match

0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 471

CF337494 20 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--07-P04.g1 AcJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--07-P04, mRNA sequence.
ACCESSION CF337494
VERSION CF337494.1 GI:33823378
KEYWORDS EST.

SOURCE

ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source
1. .20
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-P04"
/tissue_type="leaf"
/dev stage="14 days after germination"
/lab host="E.coli DH10B"
/clone lib="AcJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 472

TS0579 20 bp mRNA linear EST 06-FEB-1995
LOCUS yb76d04.r1 StrataGene ovary (#937217) Homo sapiens cDNA clone
DEFINITION IMAGE:77095 5' similar to contains 11 repetitive element, mRNA
sequence.
ACCESSION TS0579
VERSION TS0579.1 GI:652439
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 20)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisese, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W., Hawkins, M., Huleman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Merdis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Maira, M.

TITLE

Generation and analysis of 280,000 human expressed sequence tags

JOURNAL MEDLINE PUBMED

Genome Res. 6 (9), 807-828 (1996)
97044478
8889549

COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RPI
High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers

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1..20
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:506824"
/db_xref="taxon:9606"
/clone="IMAGE:77095"
/bex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/notes="Organ: ovary; Vector: B937217 SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGACGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTATTTTATTTT 3'."
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Query Match

Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy

4464 TTTTATTTTATTTTATTTT 4483
1 TTTTATTTTATTTTATTTT 20

Db

1 TTTTATTTTATTTTATTTT 20

RESULT 473

AZ307671

LOCUS

AZ307671 20 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0009M2OR Mouse 10kb plasmid UUCGM library Mus musculus genomic

clone UUCGM0009M20 R, genomic survey sequence.

ACCESSION

AZ307671

VERSION

AZ307671.1 GI:10346897

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Niederhausern, A., Rose, R., Stokes, R., Tingey, A., von

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

Unpublished (2000)

JOURNAL COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0009 row: M column: 20

Seq primer: CACACAGAAACAGCTATGAC

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers

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/notes="Vector: PMD42nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gl4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0;

Cy

4464 TTTTATTTTATTTTATTTT 4483
1 TTTTATTTTATTTTATTTT 20

Db

1 TTTTATTTTATTTTATTTT 20

RESULT 474

AZ333980

LOCUS

AZ333980 20 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0063K10F Mouse 10kb plasmid UUCGM library Mus musculus genomic

clone UUCGM0063K10 F, genomic survey sequence.

ACCESSION

AZ333980

VERSION

AZ333980.1 GI:10400856

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Niederhausern, A., Rose, R., Stokes, R., Tingey, A., von

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

plasmid inserts

Unpublished (2000)

JOURNAL COMMENT

Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: F column: 13
Seq primer: CCTGTAAACGACGCCACAT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

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/strain="C57BL/6J"
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/clone="UGC1M0076F13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 477
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DEFINITION IM0080G17R Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC1M0080G17 R, genomic survey sequence.
ACCESSION A2345856
VERSION A2345856.1 GI:10425093
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: G column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES
source

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/clone="UGC1M0080G17"
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/clone_lib="Mouse 10kb plasmid UGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4462 ACTT TTTT TTTT TTTT TTTT TTTT 4481
Db 1 ACTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 478
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DEFINITION IM0089B18F Mouse 10kb plasmid UGC1M library Mus musculus genomic
clone UGC1M0089B18 F, genomic survey sequence.
ACCESSION A2351273
VERSION A2351273.1 GI:10430510
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

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/strain="C57Bl/6J"
/db_xref="taxon:10090"
/clone="UGGCM0297E23"
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/clone_1lb="Mouse 10kb plasmid UGCM library"
/note="Vector: PMW42mV; Purified genomic DNA from M.
musculus C57Bl/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMW42 [gi|47321419b|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.8e+02;		
Matches	20;	Conservative	0;	Indels 0;
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Db       1 TTTTTTTTTTTTTTTTTT 20
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RESULT	486
AZ479464	
LOCUS	20 bp DNA
DEFINITION	linear
ACCESSION	GS5 04-OCT-2000
	1M0300P01F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
	clone UGCGIM0300P01 F, genomic survey sequence.
	AZ479464

VERSION	AZ479464.1	GI:10638941
KEYWORDS	GSS.	
SOURCE	Mus musculus	(house mou
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae; Mus-
1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00
 Plates: 0300 row: P column: 01
 Seq primer: CGTTGTAACACGCGCCAGT
 Class: plasmid ends
 High quality sequence step: 20.
 Location/Qualifiers

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/mol_type="genomic DNA"
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LOCUS	
DEFINITION	
ACCESSION	
AZ498625	20 bp DNA linear
IM0336E05F	Mouse 10kb plasmid U06C1M library Mus musculus genomic
clone U06C1M0336E05 F,	genomic survey sequence.
U06C1M0336E05 F,	
U06C1M0336E05 F,	

ACCESSION	AZ496625	GI:10676657
VERSION	AZ496625.1	
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

**REFERENCE
AUTHORS**
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0336 row: E column: 05
Seq primer: CCGTGTAAACGACGCCACG
Class: plasmid ends
High quality sequence stop: 20.

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                        /organism="Mus musculus"
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[/db_xref=taxon:10090](#)
/[clone=UUGC1M0336E05](#)
/[sex=Male](#)
/[lab_host=E. Coli strain XL10-Gold, T1-resistant, F-](#)
/[clone_1ib=Mouse 10kb plasmid UUGC1M library](#)
/[note=Vector: PM042nv; Purified genomic DNA from M. musculus C57BL/6J \(male\);](#) Purified genomic DNA from M. laboratory Mouse Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD24 (g1473211[gblAF12907.1], a copy-number inducible derivative of pAF102.R1). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.8e+02;		
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[illegible]

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LOCUS	AZ514729
DEFINITION	20 bp DNA linear GSS 05-OCT-2000
ACCESSION	U0361E11R Mouse 10kb plasmid UUCIM library Mus musculus genomic clone UUCIM0361E11 R, genomic survey sequence.
	AZ514729

VERSION	AZ514729.1	GI:10696045
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

TITLE Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A. and Wright D. Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kbp

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetice.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0361 row: E column: 11
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Clase: plasmid ends
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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
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LOCUS IM0460K05R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0460K05 R, genomic survey sequence.
ACCESSION AZ623155
VERSION AZ623155.1 GI:11745345
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiser, R.

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plasmid inserts
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: K column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

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/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
|||||
Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 494
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LOCUS IM0460L12R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
DEFINITION clone UUCG1M0460L12 R, genomic survey sequence.
ACCESSION AZ623214
VERSION AZ623214.1 GI:11745404
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellily, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiser, R.

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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0460 row: L column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0460L12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

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/notes="vector: pMD44; Purified genomic DNA from M.  

musculus C57BL/6J (male) was obtained from the Jackson  

Laboratory Mouse DNA Resource  

http://www.jax.org/resources/documents/dnares/". The DNA

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF128072.1), a copy-number inducible derivative of pAF1501. The vector was ligated with adaptors complementary to the insert adaptor and purified. The sheared, adaptorised mouse DNA was annealed to adaptorised vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.8e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

AZ760838/c		20 bp	DNA	linear	GSS 16-FEB-2001
LOCUS	AZ760838				
DEFINITION	M055A2.R Mouse 10kb plasmid UGCM library Mus musculus genomic clone UGCM055A24 R, genomic survey sequence.				

ACCESSION	AZ760838	GI:12869112
VERSION	AZ760838.1	

KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)

ORGANISM

REFERENCE
1 (bases 1 to 20)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss

University of Utah
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84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0554 row: A column: 24
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES	Location/Qualifiers
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/mol_type="genomic DNA"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWDΔ2v, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnaee/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

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1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UGGCM0560M02"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

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/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG1M0562H04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lib="Mouse 10kb plasmid UUCG1M library"
 /note="Vector: PMD4241v; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were


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1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="TUGCM0026621"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10Kb plasmid UUGCM library"
/notes="Vector: Pmd29; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passages through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt ended and repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
0.5 Kb range using preparative agarose gel

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1. 20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/sex="Male"
/lab_host="R. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1b="Mouse 10kb plasmid UUGC1 library"
/note="Vector: PWD2myc; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrolytically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 505
A2798529 20 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0655G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0055G19 F, genomic survey sequence.

ACCESSION A2798529
VERSION A2798529.1 GI:12948718
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0055 row: G column: 19

Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
SOURCE Location/Qualifiers
1..20

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g1|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483
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Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 506
A2805163 20 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0661L14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0066L14 F, genomic survey sequence.

ACCESSION A2805163
VERSION A2805163.1 GI:12965890
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0066 row: L column: 14

Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES
SOURCE Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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10.5 kb range using preparative agarose gel
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inducible derivative of plasmid R1. The vector was ligated

adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 509
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LOCUS 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0073D15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0073D15 F, genomic survey sequence.
ACCESSION
AZ809306
VERSION
AZ809306.1 GI:12975468
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0073 row: D Column: 15
Seq primer: GGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 510
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LOCUS 20 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0076120R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076120 R, genomic survey sequence.
ACCESSION
AZ810986
VERSION
AZ810986.1 GI:12978793
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: I Column: 20
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Class: plasmid ends
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

FEATURES
source
1. .20
/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

FEATURES
source
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC2M0076120"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
TTTT TTTT TTTT TTTT TTTT 1

Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 511
AZ813908/c

LOCUS

DEFINITION 20 bp DNA linear GSS 20-FEB-2001
2M0081P21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A., and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contract: Robert B. Weiss

University of Utah Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0086 row: F column: 21

Seq primer: CAGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0081P21"

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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_1ib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g14732114[gb]AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

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Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
TTTT TTTT TTTT TTTT TTTT 1

Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 512
AZ817323/c

LOCUS

DEFINITION 20 bp DNA linear GSS 20-FEB-2001
2M0086C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A., and Wright, D., Weis, R.

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84112, USA

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 1000 Std Error: 0.00

Plate: 0086 row: F column: 20

Seq primer: CACACGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

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/clone="UUGC2M0086C20"

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/clone_1ib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PMD42nv; Purified genomic DNA from M.

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Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT
 Db 20 TTTT

RESULT 513

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 LOCUS AZ817467/c
 DEFINITION 2M0086J5R Mouse 10kb plasmid UUCGM library Mus musculus genomic
 clone UUCG2M0086J5 R, genomic survey sequence.
 ACCESSION AZ817414
 VERSION AZ817414.1 GI:12987238
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0086 row: K column: 08
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0086K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gblAF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4464 TTTT
 Db 20 TTTT

RESULT 514

AZ817467 20 bp DNA linear GSS 20-FEB-2001
 LOCUS AZ817467/c
 DEFINITION 2M0086J5R Mouse 10kb plasmid UUCGM library Mus musculus genomic
 clone UUCG2M0086J5 R, genomic survey sequence.
 ACCESSION AZ817467
 VERSION AZ817467.1 GI:12987291
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausen,A. and Wright,D., Weis,R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

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 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0086 row: J column: 15
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

1.20
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0086J15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
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 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PWD42 (g14732114[gblAF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match

0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;

	Matches	Conservative	Mismatches	Indels	Gaps
Qy	4464	TTTTTTTTTTTTTTTTTTT	4483		
Dd	20	TTTTTTTTTTTTTTTTTTT	1		

RESULT 51.5

LOCUS	AZ817608	20 bp	DNA	linear	GSS 20-FEB-2001
DEFINITION	2M0087K08F Mouse 10kb plasmid library Mus musculus genomic				
DESCRIPTION	clone UUGCZM0087K08 F, genomic survey sequence.				

ACCESSION	AZ817608
VERSION	AZ817608.1
NUMBERS	GI:12987516

SOURCE ORGANISM	Mus musculus (house mouse)
Mus musculus	Mus musculus

REFERENCES

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: K column: 08
Seq primer: CGTGTAAACGACGCCAGT
Class: Plasmid ends
High quality sequence stop: 20.

FEATURES

Bouyce

/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U05C2M0087K08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UNGCM library"
 /note="Vector: pMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repeated with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (g11473111[gb]Arl29072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	4464	4483
Db	1	20

RESULT 516

LOCUS	AZ818.48R	20 bp	DNA	linear	GSS 20-FEB-2003
DEFINITION	2M0088K01	Mouse 10kb	plasmid	library	Mus musculus genomic
ACCSSION	clone UUCG2M0088K01	R,	genomic	survey	sequence.
	ctgagc480				

ACCESSION	AZ818489	
VERSION	AZ818489.1	GI:12988397
KEYWORDS	CCC	

SOURCE ORGANISM	Mus musculus (house mouse)
Mus musculus	

REFERENCE AUTHORS

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss

Kel. 308, Biomedical Polymers Research Bldg.,
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: ddamm@genetics.utah.edu
 Insert length: 1000 Std Error: 0.00
 Plate: 008 row: K column: 01
 Seq primer: CACACAGAAAACCTTGTGACC
 Class: plasmid ends
 High quality sequence stop: 20.

FEATURES

Source

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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08200088K01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lib="Mouse 10kb plasmid UGCGM library"
 /note="Vector: pMD24nv. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse Resource
 http://www.jax.org/resources/documents/dnares/. The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (g114733114[g]Afl2072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 517
 AZ818816 20 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0089M05F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG2M0089M05 F, genomic survey sequence.
 ACCESSION
 VERSION AZ818816
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0089 row: M column: 05
 Seq primer: CATTGTAAACGACGCCAGCT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES
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 1..20
 /organism="Mus musculus"
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 /strain="C57BL/6J"
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 /clone="UGCG2M0089M05"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483

Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 518
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 LOCUS
 DEFINITION 2M0132K13R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG2M0132K13 R, genomic survey sequence.
 ACCESSION
 VERSION AZ837491
 KEYWORDS
 SOURCE GSS.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
 Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0132 row: K column: 13
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers

FEATURES
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0132K13"
 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483

Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 519
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 LOCUS A2841342
 DEFINITION 2M0139H16F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGM0139H16 F, genomic survey sequence.
 ACCESSION A2841342
 VERSION A2841342.1 GI:13011250
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

TITLE
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 plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0139 row: H column: 16
 Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends

FEATURES
 source
 High quality sequence scop: 20.
 Location/Qualifiers

1..20
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 /db_xref="taxon:10090"
 /clone="UGCGM0139H16"
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 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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 of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
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Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 520
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 LOCUS A2841558
 DEFINITION 2M0139A10R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCGM0139A10 R, genomic survey sequence.
 ACCESSION A2841558
 VERSION A2841558.1 GI:13011466
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 1 (bases 1 to 20)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.

TITLE
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 plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0139 row: A column: 10
 Seq primer: CACACAGGAAACGCTATGACC
 Class: plasmid ends

FEATURES
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 High quality sequence scop: 20.
 Location/Qualifiers

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 /clone="UGCGM0139A10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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 musculus C57BL/6J (male) was obtained from the Jackson
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 (http://www.jax.org/resources/documents/dnares/). The DNA
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 polynucleotide kinase. Adaptor oligonucleotides were
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 electrophoresis. Vector DNA was prepared from a derivative
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 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464 TTTT TTTT TTTT TTTT TTTT 4483
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

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RESULT 521
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LOCUS
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ACCESSION 2M0165003P Mouse 10kb plasmid UUGC1M library Mus musculus genomic
VERSION A2858052
KEYWORDS A2858052
SOURCE A2858052.1 GI:13050813
ORGANISM Mus musculus (house mouse)
REFERENCE Mus musculus
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0163 row: 0 column: 03
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High quality sequence stop: 20.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGC2M0163003"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

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RESULT 522
A2936914/c
LOCUS
DEFINITION 20 bp DNA linear GSS 26-APR-2001
ACCESSION 2M0193G23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
VERSION A2936914
KEYWORDS A2936914
SOURCE A2936914.1 GI:13795495
ORGANISM Mus musculus (house mouse)
REFERENCE Mus musculus
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0193 row: 6 column: 23
Seq primer: CACACAGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0193G23"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 20 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 1

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RESULT 523

AZ949180
 LOCUS 20 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0212102R Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM0212102 R, genomic survey sequence.
 ACCESSION AZ949180
 VERSION 1
 KEYWORDS GI:13820407
 SOURCE
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 REFERENCE Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0212 row: 1 column: 02
 Seq primer: CACACGAGAAACGATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1..20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM0212102"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464
 1
 4483

RESULT 524
 AZ963973

AZ963973
 LOCUS 20 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M023301F Mouse 10kb plasmid UGCGM library Mus musculus genomic
 clone UGCGM023301 F, genomic survey sequence.
 ACCESSION AZ963973
 VERSION 1
 KEYWORDS GI:13835200
 SOURCE
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 REFERENCE Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0233 row: 1 column: 01
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCGM023301"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UGCGM library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464
 1
 4483

RESULT 525
 AL048777/c

AL048777

21 bp

mRNA

linear

EST 04-SEP-2003

DEFINITION DKFZp566N053_r1.566 (synonym: hfk42) Homo sapiens cDNA clone
ACCESSION DKFZp566N053, mRNA sequence.
VERSION AL048777
KEYWORDS EST, GI:4727848
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE 1 (bases 1 to 21)
JOURNAL Euphrat, et al.
COMMENT Unpublished (1999)
MIPS Contact: MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source
1..21
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566N053"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfk42)"
/note="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
|||||
Db 21 TTTT TTTT TTTT TTTT TTTT 2

RESULT 526 21 bp mRNA linear EST 10-OCT-2003
BX556006
LOCUS BX556006 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone tse24c09_p1c, mRNA sequence.
ACCESSION BX556006
VERSION BX556006.1 GI:33379965
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 21)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
location/Qualifiers
1..21

FEATURES
source
1..21

/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="tse24c09_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483
|||||
Db 2 TTTT TTTT TTTT TTTT TTTT 21

RESULT 527 21 bp mRNA linear EST 10-OCT-2003
BX558161
LOCUS BX558161 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone tse37a05_p1c, mRNA sequence.
ACCESSION BX558161
VERSION BX558161.1 GI:33429302
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 21)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
location/Qualifiers
1..21

FEATURES
source
1..21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="tse37a05_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTT TTTT TTTT TTTT TTTT 4485
|||||

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 531

CF295642

LOCUS 30DGS--05-K20.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza

DEFINITION sative cDNA clone 30DGS--05-K20, mRNA sequence.

ACCESSION CF295642

VERSION CF295642.1 GI:33664675

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--05-K20"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 532

CF297615

LOCUS 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza

DEFINITION sative cDNA clone 30DGS--08-J10, mRNA sequence.

ACCESSION CF297615

VERSION CF297615.1 GI:33666648

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--08-J10"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 21 TTTT TTTT TTTT TTTT TTTT 2

RESULT 533

CF298322

LOCUS 30DGS--01-K14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sative cDNA clone 7LEAF--01-K14, mRNA sequence.

ACCESSION CF298322

VERSION CF298322.1 GI:33670083

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

SOURCE

1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--01-K14"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_1lb="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 534
 CF310809
 LOCUS 7LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION
 ACCESSION CF310809
 VERSION CF310809.1 GI:33672570
 KEYWORDS EST
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzaceae; Oryza.
 1 (bases 1 to 21)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--05-G20"
 /rissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 535
 CF312715
 LOCUS ABF--08-J10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--08-J10, mRNA sequence.
 ACCESSION CF312715
 VERSION CF312715.1 GI:33684476
 KEYWORDS EST
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzaceae; Oryza.
 1 (bases 1 to 21)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF--08-J10"
 /rissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid
 cDNA library (ABF)"
 /note="Vector: pCR4-TOPO, Site_1: EcoRI; leaf was dried
 for 2hrs. Oligo-capped mRNA was reverse transcribed and
 then used for PCR. mRNA was prepared from ABA-responsive
 element binding transcription factor 3 overexpression
 line."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 21 TTTT TTTT TTTT TTTT TTTT 2

RESULT 536
 CF316073
 LOCUS HD--05-D16.b1 OshDACL-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (HD) Oryza sativa cDNA clone HD--05-D16, mRNA sequence.
 ACCESSION CF316073
 VERSION CF316073.1 GI:33687834
 KEYWORDS EST
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzaceae; Oryza.
 1 (bases 1 to 21)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--05-D16"
 /rissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OshDACL-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO, Site_1: EcoRI; Callus was

/lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 540
 CF338057/c
 LOCUS
 DEFINITION JMT--08-M03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
 library (JMT) Oryza sativa cDNA clone JMT--08-M03, mRNA sequence.
 CF338057
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

1. (bases 1 to 21)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers
 1. 21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--08-M03"
 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 21 TTTT TTTT TTTT TTTT TTTT TTTT 2

RESULT 541
 CF338522
 LOCUS
 DEFINITION RCL1--01-P04.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa cDNA clone RCL1--01-P04, mRNA sequence.

21 bp mRNA linear EST 18-AUG-2003
 RCL1--01-P04.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa cDNA clone RCL1--01-P04, mRNA sequence.

1. (bases 1 to 21)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers
 1. 21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--08-M03"
 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid
 cDNA library (JMT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
 was reverse transcribed and then used for PCR. mRNA was
 prepared from Arabidopsis Jasmonate Carboxyl
 methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 21 TTTT TTTT TTTT TTTT TTTT TTTT 2

RESULT 541
 CF338522
 LOCUS
 DEFINITION RCL1--01-P04.g1 Regenerated callus lambda phage cDNA library (RCL1)
 Oryza sativa cDNA clone RCL1--01-P04, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzae; Oryza.

1. (bases 1 to 21)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers
 1. 21
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="RCL1--01-P04"
 /tissue_type="callus"
 /dev_stages="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli SOLR"
 /clone_lib="Regenerated callus lambda phage cDNA library
 (RCL1)"
 /note="Vector: pBlueScript SK(+); Site 1: SclI; Site 2:
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'
 end with SclI and 3' end with XhoI site. Callus was
 induced on 2N6 media for 30 days and cultured for 36hrs on
 regenerated media"

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 542
 AZ348593/c
 LOCUS
 DEFINITION 1M0085A13F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0085A13 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606

Location/Qualifiers
 1. 21
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /clone="UUC1M0085A13 F, genomic survey sequence"

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 542
 AZ348593/c
 LOCUS
 DEFINITION 1M0085A13F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0085A13 F, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 21)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES
source

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1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0149A13"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
      |||||
Db 21 TTTT TTTT TTTT TTTT TTTT TTTT 2
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RESULT 547

AZ389687/c

LOCUS

DEFINITION 1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0150B10 R, genomic survey sequence.

ACCESSION AZ389687

VERSION AZ389687.1 GI:10503395

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0150 row: B column: 10

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

FEATURES
source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUGC1M0150B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
      |||||
Db 21 TTTT TTTT TTTT TTTT TTTT TTTT 2
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RESULT 548

AZ406936

LOCUS

DEFINITION 1M0176E24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0176E24 F, genomic survey sequence.

ACCESSION AZ406936

VERSION AZ406936.1 GI:10530949

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0176 row: E column: 24

Seq primer: CGTTGTAAAAACGACGCCAGT

Class: plasmid ends

/lab_host="E. Coli strain X10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCim library"
/note="vector: pWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114[gb]AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli X10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
Db 1 TTTTTTTTTTTTTTTTTT 20

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RESULT	558
ACCESSION	AZ627845
LOCUS	AZ627845
DEFINITION	1M0474G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474G11 F, genomic survey sequence.
ACCESSION	AZ627845
VERSION	AZ627845.1 GI:11750131
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 21) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA Tel.: 801.595.5606

```

Email: daunnegenetics.utan.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: G column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
      Location/Qualifiers
1..21
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  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0474G11"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

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/clone_lib="Mouse 10kb plasmid UUGCIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 559
 AZ657727/c 21 bp DNA linear GSS 14-DEC-2000
 LOCUS
 DEFINITION IM0534B07F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0534B07 F, genomic survey sequence.

ACCESSION AZ657727

VERSION AZ657727.1 GI:11794873

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0534 row: 0 column: 07

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0534B07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
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 Db 21 TTTT TTTT TTTT TTTT TTTT TTTT 2

RESULT 560
 AZ766552/c 21 bp DNA linear GSS 16-FEB-2001

LOCUS
 DEFINITION IM0564O11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0564O11 F, genomic survey sequence.

ACCESSION AZ766552

VERSION AZ766552.1 GI:12883741

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 21)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0564 row: 0 column: 11

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCIM0564O11"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGCIM library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

Laboratory Mouse DNA Resource

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gels electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

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Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4464 TTTTTTTTTTTTTTTTTT 4483
Dd 21 TTTTTTTTTTTTTTTTTT 2

RESULT 564	21 bp	DNA	linear	GSS 20-FEB-2001
AZ810054	10kb	plasmid	UUGC1M library	Mus musculus genomic
LOCUS	2M0074E19F	Mouse	2M0074E19 F.	genomic survey sequence.
DEFINITION	clone	UUGC2M0074E19		

ACCESSION	AZ810054
VERSION	AZ810054.1
KEYWORDS	GI:12976935
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
	1 (bases 1 to 21)
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.. Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUc, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0074 row: E column: 19
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

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FEATURES
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                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGCIM library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                    musculus C57BL/6J (male) was obtained from the Jackson
                    Laboratory Mouse DNA Resource
                    (http://www.jax.org/resources/documents/dnares/). The DNA
                    was hydrodynamically sheared by repeated passage through a

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was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%  Score 20;  DB 1;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 2e+02;
Matches 20;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  4464  TTTTTTTTTTTTTTTTTTTT 4483
Db   21  TTTTTTTTTTTTTTTTTTTT 2

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RESULT	566
AZ819181/c	
LOCUS	
DEFINITION	AZ819181 2M00989110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0089110 R, genomic survey sequence.
	21 bp DNA linear GSS 20-FEB-2001

VERSION	AZ819181.1	GI:12983089
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 21)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,M., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: I column: 10
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

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FEATURES
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/clone="UUC2M0089110"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0228A01"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pWP42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to

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/organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
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 /clone="UUGC2M0288020"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnarse/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel

RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 574
 CF332379
 LOCUS
 DEFINITION NACL--08-N21.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa CDNA clone NACL--08-N21, mRNA sequence.
 ACCESSION CF332379
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

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 1. .23
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
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 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 575
 CF334077
 LOCUS
 DEFINITION JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa CDNA clone JMT--03-D17, mRNA sequence.
 ACCESSION CF334077
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University
 Yongsin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
 1. .23
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="JMT--03-D17"
 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
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 Db 3 TTTT TTTT TTTT TTTT TTTT TTTT 22

RESULT 576

AL587718
 LOCUS
 DEFINITION AL587718 BP Chicken Brain Library Gallus gallus cDNA clone ROS061C02, mRNA sequence.
 ACCESSION AL587718
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Gallus gallus (chicken)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

Query Match 0.3%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
 |||||
 Db 3 TTTT TTTT TTTT TTTT TTTT TTTT 22

REFERENCE
 AUTHORS Murray, F.
 TITLE BP Chicken Brain Library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Frazer Murray
 Dept. Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UK
 Tel: +44 (0)131 527 4200
 Fax: +44 (0)131 440 0434
 Email: frazer.murray@roscire.ac.uk
 GCGGCGCTTTT TTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (#6854-)

FEATURES

source
 1. .25
 /organism="Gallus gallus"
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 /tissue_type="Brain"
 /dev_stage="Unknown"


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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: F column: 09
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
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/clone="UUC1M0056F09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
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RESULT 580
BQ583199
LOCUS
DEFINITION
E012097-024-006-E10-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-006-E10 5-PRIME, mRNA sequence.
ACCESSION
BQ583199
VERSION
BQ583199.1 GI:26112776
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 26)

REFERENCE
AUTHORS
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 26 Std Error: 0.00
Plate: 6 row: E column: 10
Seq primer: SP6; CATACGATTTAGTGACACTATAG.

FEATURES
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/cultivar="KWS2320 (double haploid, monogerm breeding
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/db_xref="GABI:183502"
/db_xref="taxon:161934"
/clone="024-006-E10"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung. Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 20; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 581
AZ358846
LOCUS
DEFINITION
1M0101M24F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0101M24 F, genomic survey sequence.
ACCESSION
AZ358846
VERSION
AZ358846.1 GI:10472546
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)

REFERENCE
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss

```

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0101 row: M column: 24
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES

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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0101M24"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4463

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 582

CF310560

LOCUS

DEFINITION ABF--05-E14_b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--05-E14, mRNA sequence.

ACCESSION

CF310560

VERSION

CF310560.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 27)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .27
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 27;

Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4465 TTTT TTTT TTTT TTTT TTTT TTTT 4484

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 583

CF333518

LOCUS

DEFINITION JMT--02-H05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-H05, mRNA sequence.

ACCESSION

CF333518

VERSION

CF333518.1

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 27)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .27

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="JMT--02-H05"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"

/note="Vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match

0.3%; Score 20; DB 1; Length 27;


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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4483
Db 1 TTTT... 20

RESULT 584
CF334654
LOCUS
DEFINITION JMT--04-A12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--04-A12, mRNA sequence.
ACCESSION CF334654
VERSION
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnah@gbio.com, bhnah@bio.myongji.ac.kr.

FEATURES
source
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clones="JMT--04-A12"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4483
Db 1 TTTT... 20

RESULT 585
N34515
LOCUS
DEFINITION Y555b01.s1 Soares multiple sclerosis 2NbHMSp Homo sapiens cDNA
clone IMAGE:277510 3' similar to gb:578694 PROTEIN-LYSINE 6-OXIDASE
PRECUSOR (HUMAN); mRNA sequence.
ACCESSION N34515
VERSION N34515.1 GI:1155657
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 27)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfs,T., Soares,M., Tan,F.,
Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
1..27
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3895793"
/db_xref="taxon:9606"
/clones="IMAGE:277510"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares multiple sclerosis 2NbHMSp"
/notes="vector: p773D (Pharmacia) with a modified
polylinker V-type phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5',
TGTACCAATCTGAAGTGGAGCGCGCCATTTT...TTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."

Query Match 0.3%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4483
Db 1 TTTT... 20

RESULT 586
AZ382581
LOCUS
DEFINITION AZ382581 Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0139120 R, genomic survey sequence.
ACCESSION AZ382581
VERSION
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

```

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: I column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0139120"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTT 4482
|||||
Db 8 CTTTTTTTTTTTTTTTTT 27

RESULT 587
AZ654007
LOCUS 28 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0527020R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0527020 R, genomic survey sequence.

ACCESSION AZ654007
VERSION 1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0527 row: O column: 20
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28.

FEATURES
source
1. .28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0527020"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTTTTTTTTTTTTTCT 4485
|||||
Db 8 TTTTTTTTTTTTTTTTGT 27

RESULT 588
AL048694/C
LOCUS 29 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZP566D043_r1 566 (synonym: hfk2d) Homo sapiens cDNA clone DKFZP566D043, mRNA sequence.

ACCESSION AL048694
VERSION 1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 29)
Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
EST (Koehrer, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

```

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFP566J063"
        /tissue_type="kidney"
        /dev_stage="fetal"
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        /clone_lib="566 (synonym: hfkd2)"
        /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match
  Best Local Similarity 0.3%; Score 20; DB 1; Length 29;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 29 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 10

RESULT 589
AL048741/C 29 bp mRNA linear EST 04-SEP-2003
LOCUS
DEFINITION DKFP566J063_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION DKFP566J063, mRNA sequence.
VERSION AL048741
KEYWORDS EST.
SOURCE AL048741.1 GI:4727812
  ORGANISM Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 29)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="DKFP566J063"
        /tissue_type="kidney"
        /dev_stage="fetal"
        /lab_host="X1-2blue"
        /clone_lib="566 (synonym: hfkd2)"
        /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match
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  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
Db 29 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 10

RESULT 590
CF292082 29 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION 14ROOT--02-M08.b1 Rice root plasmid cDNA library (14ROOT) Oryza
  sativa cDNA clone 14ROOT--02-M08, mRNA sequence.
ACCESSION CF292082
VERSION CF292082.1 GI:33661115
KEYWORDS EST.
SOURCE Oryza sativa
  ORGANISM Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Oryza sativa"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
        /clone="30DGS--05-E14"
        /tissue_type="leaf"
        /dev_stage="30 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE
  AUTHORS
  TITLE
  JOURNAL
  COMMENT

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Oryza sativa"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
        /clone="14ROOT--02-M08"
        /tissue_type="root"
        /dev_stage="14 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice root plasmid cDNA library (14ROOT)"
        /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
        with oligoribonucleotides and then used as templates for
        RT-PCR."

Query Match
  Best Local Similarity 0.3%; Score 20; DB 1; Length 29;
  Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4455 GGCA TGGT GACT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 2 GGCA TGGT GACT GTTT TTTT TTTT TTTT TTTT TTTT TTTT 29

RESULT 591
CF295370 29 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION 30DGS--05-E14.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
  sativa cDNA clone 30DGS--05-E14, mRNA sequence.
ACCESSION CF295370
VERSION CF295370.1 GI:33664403
KEYWORDS EST.
SOURCE Oryza sativa
  ORGANISM Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Oryza sativa"
        /mol_type="mRNA"
        /cultivar="Nackdong"
        /db_xref="taxon:4530"
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        /tissue_type="leaf"
        /dev_stage="30 days after germination"
        /lab_host="E.coli DH10B"
        /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"

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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4456 GCATGACACTTTTCTTTTCTTTTCTTTTCTTTT 4483
||||| | | | | | | | | | | | | | | | | | | | |
Db 1 GCATGACAGTGTCTTTTCTTTTCTTTTCTTTTCTTTT 28

RESULT 592
CF295445
LOCUS
DEFINITION
30DGS--05-G12-g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-G12, mRNA sequence.

CF295445
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .29
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--05-G12"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4455 GGCATGACACTTTTCTTTTCTTTTCTTTTCTTTT 4482
||||| | | | | | | | | | | | | | | | | | | | |
Db 2 GGCATGACAGTGTCTTTTCTTTTCTTTTCTTTTCTTTT 29

RESULT 593
CF306409/c
LOCUS
DEFINITION
HDAL--03-M04.g1 OshDACL1-overexpressing transgenic rice lambda phage cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-M04, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CF306409
EST.
Oryza sativa
Oryza sativa

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .29
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAL--03-M04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDACL1-overexpressing transgenic rice lambda phage cDNA library I (HDAL)"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 4.3e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4455 GGCATGACACTTTTCTTTTCTTTTCTTTTCTTTT 4482
||||| | | | | | | | | | | | | | | | | | | | |
Db 28 GGGGGGGGGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 594

TA239G06Q/c

LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 239g06, reverse sequence, genomic survey sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AL481179
GI:11846878
GSS.
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

AUTHORS

1 (bases 1 to 29)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

TITLE

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES

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1..29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="239g06"

Query Match 0.3%; Score 20; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 4463 CTTTTTTTTTTTTTTTTT 4482
|||||
Db 20 CTTTTTTTTTTTTTTTTT 1

RESULT 595
AL048729/c
LOCUS
DEFINITION DKZP5661113.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
30 bp mRNA linear EST 04-SEP-2003
ACCESSION AL048729
VERSION AL048729.1 GI:4727800
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
1 (bases 1 to 30)
EST (Koehler, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES

source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="DKFZp5661113"
/tissue type="kidney"
/dev stages="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"

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Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
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Db 30 TTTTTTTTTTTTTTTTTT 11

RESULT 596
BX551781
LOCUS
DEFINITION BX551781 Glossina morsitans morsitans adult infected gut Glossina
30 bp mRNA linear EST 10-OCT-2003
morsitans morsitans cDNA clone Tseilg01_plc, mRNA sequence.

ACCESSION BX551781
VERSION BX551781.1 GI:33376108
KEYWORDS EST.
SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 30)

AUTHORS

TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
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/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tseilg01_plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 4465 TTTTTTTTTTTTTTTT 4484
|||||
Db 11 TTTTTTTTTTTTTTTT 30

RESULT 597

BX553141

LOCUS

DEFINITION BX553141 Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tseil27e12_plc, mRNA sequence.

VERSION BX553141

KEYWORDS BX553141.1 GI:33377334

SOURCE EST.

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 30)

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES

source
Location/Qualifiers
1. 30
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4465 TTTTCTTTTCTTTCTTTG 4484

Db 11 TTTTCTTTTCTTTCTTTG 30

RESULT 598

CF333289
LOCUS
DEFINITION
JMT--02-C01.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-C01, mRNA sequence.

CF333289

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1. (bases 1 to 30)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongui University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
Location/Qualifiers
1. 30
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-C01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"
/note="vector: PCR4-TOP0; Site_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 4.7e+02;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTCTTTG 4491

|||||

Db

RESULT 599

AZ604126/c

LOCUS

DEFINITION

clone UUGC1M0423013 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. 30

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0423013"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.7e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5699 TTTGCTTCTTTCTTTCTTTCTTTT 5726

|||||

Db 29 TTTGCTTCTTTCTTTCTTTCTTTT 2

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Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-01-G01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 1 TTTTTCCTTTTTCCTTTTTCCTTC 23

RESULT 602
CF313297
LOCUS
DEFINITION
HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. 23
/organism="Oryza sativa"
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(14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 1 TTTTTCCTTTTTCCTTTTTCCTTC 23

RESULT 601
CF313297
LOCUS
DEFINITION
HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. 23
/organism="Oryza sativa"
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/cultivar="Nackdong"
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/clone="HD-01-G01"
/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 1 TTTTTCCTTTTTCCTTTTTCCTTC 23

RESULT 601
CF313297
LOCUS
DEFINITION
HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 1 TTTTTCCTTTTTCCTTTTTCCTTC 23

RESULT 601
CF313297
LOCUS
DEFINITION
HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="HD-01-G01"
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/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 1 TTTTTCCTTTTTCCTTTTTCCTTC 23

RESULT 601
CF313297
LOCUS
DEFINITION
HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnamh@bio.com, bhnamh@bio.myongji.ac.kr.

FEATURES
source
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD-01-G01"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTC 4486
|||||
DB 1 TTTTTCCTTTTTCCTTTTTCCTTC 23

RESULT 601
CF313297
LOCUS
DEFINITION
HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji
```



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Query Match      0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT...TTTTTGCT 4487
DB 1 TTTT...TTTTTGCT 23

RESULT 603
AZ607198/c
LOCUS
DEFINITION
  AZ607198 Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0429G03 R, genomic survey sequence.
ACCESSION
  AZ607198
VERSION
  AZ607198.1 GI:11729388
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 24)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0429 row: G column: 03
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 24.
  Location/Qualifiers
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      /mol_type="genomic DNA"
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      /db_xref="taxon:10090"
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      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: pWd42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWd42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT...TTTTTGCT 4487
DB 1 TTTT...TTTTTGCT 23

RESULT 603
AZ607198/c
LOCUS
DEFINITION
  AZ607198 Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0429G03 R, genomic survey sequence.
ACCESSION
  AZ607198
VERSION
  AZ607198.1 GI:11729388
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 24)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE
  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0429 row: G column: 03
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 24.
  Location/Qualifiers
    1..24
      /organism="Mus musculus"
      /mol_type="genomic DNA"
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      /clone="UUGC1M0429G03"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: pWd42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWd42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 3.e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT...TTTTTGCT 4487
DB 24 TTTT...TTTTTAATT 2

RESULT 604
CF326989
LOCUS
DEFINITION
  CF326989 Rice callus plasmid cDNA library (NACL) Oryza sativa CDNA clone NACL--01-E15, mRNA sequence.
ACCESSION
  CF326989
VERSION
  CF326989.1 GI:33802233
KEYWORDS
  EST.
SOURCE
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
  Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
JOURNAL
  Unpublished (2003)
COMMENT
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
  Location/Qualifiers
    1..25
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
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      /clone="NACL--01-E15"
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      /dev_stage="proliferated callus on 2N6 media for 30 days"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice callus plasmid cDNA library (NACL)"
      /note="Vector: PCR4-TOPO; site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.3%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 3.e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4466 TTTT...TTTTTGCT 4488
DB 1 TTTT...TTTTTCTCT 23

RESULT 605
AZ774476/c
LOCUS
DEFINITION
  AZ774476 Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004A01 F, genomic survey sequence.
ACCESSION
  AZ774476
VERSION
  AZ774476.1 GI:12899965
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 25)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
```

TITLE	JOURNAL	JOURNAL MEDIAN PUBLISHED COMMENT
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center		

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1. 28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tss1906 plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T. brucei"

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Query Match

KEYWORDS
SOURCE
ORGANISM

Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocarpaceae; Oryzaceae; Oryza.

1. (Bases 1 to 29)
Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K. and Nahm, B. H. Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)
Contact: Nahm B. H.

Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@qbio.com, bhnahm@bio.myongji.ac.kr.

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Email: binhan@go.ri.ac.kr.
Location/Qualifiers
1. .29
/organism="Oryza sativa"
/mol type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--03-B05"
/tissue type="leaf"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="3DGS-03-B05"
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/dev stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19.8; DB 1; Length 29;
Best Local Similarity 91.3%; Pred. No. 4.7e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTTTTGG 4484
Db 7 AGTGTGTGTGTGTGTGTGTGTGTG 29

RESULT 608
LOCUS N31821 30 bp mRNA linear EST 10-JAN-1996
DEFINITION YY17912.s1 Soares melanocyte 2N5HM Homo sapiens cDNA clone
IMAGE:271558 3' similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
HIN-1 (HUMAN); mRNA sequence.
ACCESSION N31821
VERSION N31821.1 GI:1152220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 30)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: ml3 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
1..30
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/mol_type="mRNA"
/db_xref="GDB:3881200"
/db_xref="taxon:9606"
/clone="IMAGE:271558"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2N5HM"
/notes="Vector: pT73D (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCACTCAAGTCGAGCGGCGGCGAGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

/dev stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19.8; DB 1; Length 30;
Best Local Similarity 84.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4466 TTTTTTTTTTTTTTTTTTCTCTTGA 4490
Db 1 TTTTTTTTTTTTTTTTTTCTTGA 25

RESULT 609
LOCUS CF300765 27 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-F21, mRNA sequence.
ACCESSION CF300765
VERSION CF300765.1 GI:33672526
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
of Bioscience and Genetics Institute, GreenGene Biotech Inc.; Division
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..27
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/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19.6; DB 1; Length 27;
Best Local Similarity 84.6%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTGTCTTG 4489
Db 1 TTTTTTTTTTTTTTAATTATTG 26

RESULT 610
LOCUS BX551339 29 bp mRNA linear EST 10-OCT-2003
DEFINITION BX551339 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tseil8a05_p1c, mRNA sequence.
ACCESSION BX551339
VERSION BX551339.1 GI:33375364
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE 1 (bases 1 to 29)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

```


RESULT	618
AZ493766/c	
LOCUS	AZ493766/c
DEFINITION	AZ493766
ACCESSION	AZ493766
VERSION	AZ493766.1
KEYWORDS	GI:10667750
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
	Bekarvota; Euteleostomi;
	linear GSS 05-OCT-2000
	21 bp DNA
	1M0328C11R Mouse 10kb plasmid UUCGM library Mus musculus genomic
	clone UUCGM0328C11 R, genomic survey sequence.


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Db      1  TTTTTCCTTTTTCCTTTTCCTTC 21

RESULT 621
AL587621
LOCUS   AL587621      23 bp  mRNA      linear      EST 02-MAR-2001
DEFINITION BP Chicken Brain Library Gallus gallus cDNA clone
            ROS059H07, mRNA sequence.
ACCESSION AL587621.1  GI:13192655
VERSION   AL587621
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
JOURNAL   Phasianinae; Gallus.
COMMENT   1. (bases 1 to 23)
            Murray, F.
            BP Chicken Brain Library
            Unpublished (2001)
            Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbarc.ac.uk
            GCGGCCGCTTTTTCCTTTTTCCTTC 3' Poly A RNA purchased from Clontech
            (*6854-
            Seq primer: M13F.
            Location/Qualifiers
            1..23
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            /dev_stage="Unknown"
            /lab_host="DH10B"
            /clone_lib="BP Chicken Brain Library"
            /note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI; Cloned
            unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
            5' TGACCTCGAG 3' ; 3' adaptor sequence: 5'
            GCGGCCGCTTTTTCCTTTTTCCTTC 3' Poly A RNA purchased from
            Clontech (*6854-1)"

FEATURES
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            Location/Qualifiers
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            /strain="C57BL/6J"
            /db_xref="taxon:10090"
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            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.3%; Score 19.4; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACTTTTTCCTTTTTCCTTTTTCCTTC 4483
      |||
      1 AATTTCCTTTTTCCTTTTTCCTTC 22

Db

RESULT 622
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LOCUS   AL587621      24 bp  DNA      linear      GSS 13-DEC-2000
DEFINITION IM0466J07F Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUC1M0466J07 F, genomic survey sequence.
ACCESSION AL587621
VERSION   AL587621.1  GI:11748291
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1. (bases 1 to 24)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb

TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0466 row: J column: 07
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
            Location/Qualifiers
            1..24
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUC1M0466J07"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.3%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4463 CTTTTCCTTTTTCCTTTTTCCTTC 4483
      |||
      3 CTTTTCCTTTTTCCTTTTTCCTTC 23

Db

RESULT 623
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LOCUS   AL587621      24 bp  DNA      linear      GSS 16-FEB-2001
DEFINITION IM0560H02R Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUC1M0560H02 R, genomic survey sequence.
ACCESSION AL587621
VERSION   AL587621.1  GI:12879519
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1. (bases 1 to 24)
            Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
            Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
            Niederhausern, A. and Wright, D., Weiss, R.
            Mouse whole genome scaffolding with paired end reads from 10kb

```

```

JOURNAL
COMMENT
    plasmid inserts
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0560 row: H column: 02
    Seq primer: CACACAGAAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 24.
    Location/Qualifiers
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    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0560H02"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match 0.3%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTT 4482
Db 21 AATTTTCTTTTCTTTTCTTTT 1

RESULT 624
AZ764513/c 24 bp DNA linear GSS 16-FEB-2001
LOCUS
DEFINITION
    clone UUGC1M0560D11 R, genomic survey sequence.
ACCESSION
    AZ764513
VERSION
    AZ764513.1 GI:12879553
KEYWORDS
    GSS.
SOURCE
    Mus musculus (house mouse)
ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1 (bases 1 to 24)
REFERENCE
    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
    Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
    Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
    Niederhausern, A. and Wright, D., Weiss, R.
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts

JOURNAL
COMMENT
    Unpublished (2000)
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0560 row: D column: 11
    Seq primer: CACACAGAAACAGCTATGACC
    Class: plasmid ends
    High quality sequence stop: 24.
    Location/Qualifiers
    1. .24
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0560D11"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match 0.3%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTT 4482
Db 21 AATTTTCTTTTCTTTTCTTTT 1

RESULT 625
AV737092/c 25 bp mRNA linear EST 17-OCT-2000
LOCUS
DEFINITION
    AV737092 CB Homo sapiens cDNA clone CBFIB11 5', mRNA sequence.
ACCESSION
    AV737092
VERSION
    AV737092.1 GI:10854673
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 25)
REFERENCE
    Zhang, Q., Ye, M., Wu, X., Gu, J., Huang, Q., Zhou, J., Shen, Y., Han, Z.,
    Chen, S., Mao, M. and Chen, Z.
    Homo sapiens CB library cDNA clones
    Unpublished (2000)
    Contact: Zhu Chen
    Shanghai Institute of Hematology, Rui-Jin Hospital
    197 Rui-Jin II Road, Shanghai 200025, P. R. China
    Tel: 86-21-64740490

```

```

Fax: 86-21-64743206
Email: mbshims.stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
1. .25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFB1B11"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/notes="Vector: pBluescript; Site 1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTT 4485
Db 25 TTTTCTTTTCTTTTCTTTTCTT 4

RESULT 626
TA388E06P/c 25 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 388e06, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL498782
VERSION AL498782.1 GI:11874504
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
REFERENCE Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
1 (bases 1 to 25)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 Kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. .25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="388e06"

FEATURES
source

Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES
source

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Qy 4463 CTTTCTTTTCTTTTCTTTTCTT 4483
Db 21 CTTCTTTTCTTTTCTTTTCTT 1

RESULT 627
CF309933/c 26 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--04-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--04-F09, mRNA sequence.
ACCESSION CF309933
VERSION CF309933.1 GI:33681694
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-F09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.3%; Score 19.4; DB 1; Length 26;
Best Local Similarity 95.2%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTCTT 4482
Db 21 AGTTTCTTTTCTTTTCTTTTCTT 1

RESULT 628
AZ764502/c 26 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0560L03R Mouse 10kb plasmid UGCM1 library Mus musculus genomic
DEFINITION clone UGCM1M0560L03 R, genomic survey sequence.
ACCESSION AZ764502
VERSION AZ764502.1 GI:12879531
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, S., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

```

TITLE Niederhauser, A. and Wright, D., Weiss, R.
JOURNAL Mouse whole genome scaffolding with paired end reads from 10kb
COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0560 row: L column: 03
 Seq primer: CACACAGGAACACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 26.

FEATURES
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0560L03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19.4; DB 1; Length 26;
 Best Local Similarity 95.2%; Pred. No. 4.3e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTT 4482
 Db 21 AATTTTTTTTTTTTTTTT 1

RESULT 629
LOCUS BX554747 28 bp mRNA linear EST 10-OCT-2003
DEFINITION morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse17c01_plc, mRNA sequence.

ACCESSION BX554747
VERSION BX554747.1 GI:33378810
KEYWORDS EST.

SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune response genes
 Genome Biol. 4 (10), R63 (2003)
 22881942
 14519198
COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
 Location/Qualifiers
 1. .28
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse17c01_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected gut"
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 28;
 Best Local Similarity 95.2%; Pred. No. 5e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTT 4484
 Db 8 TGTGTGTGTGTGTGTGTGT 28

RESULT 630
LOCUS BX555569

DEFINITION BX555569 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21e01_plc, mRNA sequence.

ACCESSION BX555569
VERSION BX555569.1 GI:33379552
KEYWORDS EST.

SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198

COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 29)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

AUTHORS
TITLE Contact: Robert Strausberg, Ph.D.
JOURNAL Email: cgapbs-x@mail.nih.gov
COMMENT Tissue Procurement: ATCC
CDNA Library Preparation: Edge Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: NIH Intramural Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bhrp/image/image.html
Plate: LLCM028 row: L column: 18
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
1..29
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2846753"
/tissue_type="T cell leukemia"
/cell_line="MGC2"
/clone_lib="NIH_MGC_2"
/notes="Organ: Blood; Vector: pOTB7a; Library prepared by
Edge Biosystems."

FEATURES
source
Query Match 0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 4466 TTTTGTGTC 4486
|||||
Db 29 TTTTGTGTC 9

RESULT 633
BX549814
LOCUS BX549814 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans CDNA clone Tse10C03_plc, mRNA sequence.
BX549814 29 bp mRNA linear EST 10-OCT-2000
BX549814 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans CDNA clone Tse10C03_plc, mRNA sequence.
BX549814.1 GI:33369063
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qic are reverse primer reads starting at 5'

Matches	20;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	4462	ACTTTTTTTTTTTTTTTTTT	4482						
Db	9	AGTTTTTTTTTTTTTTTTTT	29						
RESULT 635									
LOCUS	29 bp	mrna	linear	EST 10-OCT-2003					
DEFINITION	29 bp	mrna	linear	EST 10-OCT-2003					
ACCESSION	29 bp	mrna	linear	EST 10-OCT-2003					
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KEYWORDS	29 bp	mrna	linear	EST 10-OCT-2003					
SOURCE	29 bp	mrna	linear	EST 10-OCT-2003					
ORGANISM	29 bp	mrna	linear	EST 10-OCT-2003					
REFERENCE	29 bp	mrna	linear	EST 10-OCT-2003					
AUTHORS	29 bp	mrna	linear	EST 10-OCT-2003					
TITLE	29 bp	mrna	linear	EST 10-OCT-2003					
JOURNAL	29 bp	mrna	linear	EST 10-OCT-2003					
MEDLINE	29 bp	mrna	linear	EST 10-OCT-2003					
PUBMED	29 bp	mrna	linear	EST 10-OCT-2003					
COMMENT	29 bp	mrna	linear	EST 10-OCT-2003					
FEATURES	29 bp	mrna	linear	EST 10-OCT-2003					
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/tissue_type="adult infected gut"	29 bp	mrna	linear	EST 10-OCT-2003					
/clone_lib="Glossina morsitans morsitans adult infected gut"	29 bp	mrna	linear	EST 10-OCT-2003					
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"	29 bp	mrna	linear	EST 10-OCT-2003					
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Best Local Similarity	29 bp	mrna	linear	EST 10-OCT-2003					
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Qy	4462	ACTTTTTTTTTTTTTTTTTT	4482						
Db	9	AGTTTTTTTTTTTTTTTTTT	29						
RESULT 636									
LOCUS	29 bp	mrna	linear	EST 10-OCT-2003					
DEFINITION	29 bp	mrna	linear	EST 10-OCT-2003					
ACCESSION	29 bp	mrna	linear	EST 10-OCT-2003					
VERSION	29 bp	mrna	linear	EST 10-OCT-2003					
KEYWORDS	29 bp	mrna	linear	EST 10-OCT-2003					
SOURCE	29 bp	mrna	linear	EST 10-OCT-2003					
ORGANISM	29 bp	mrna	linear	EST 10-OCT-2003					
REFERENCE	29 bp	mrna	linear	EST 10-OCT-2003					
AUTHORS	29 bp	mrna	linear	EST 10-OCT-2003					
TITLE	29 bp	mrna	linear	EST 10-OCT-2003					
JOURNAL	29 bp	mrna	linear	EST 10-OCT-2003					
MEDLINE	29 bp	mrna	linear	EST 10-OCT-2003					
PUBMED	29 bp	mrna	linear	EST 10-OCT-2003					
COMMENT	29 bp	mrna	linear	EST 10-OCT-2003					
FEATURES	29 bp	mrna	linear	EST 10-OCT-2003					
source	29 bp	mrna	linear	EST 10-OCT-2003					
Location/Qualifiers	29 bp	mrna	linear	EST 10-OCT-2003					
1..29	29 bp	mrna	linear	EST 10-OCT-2003					
/organism="Glossina morsitans morsitans"	29 bp	mrna	linear	EST 10-OCT-2003					
/mol_type="mrna"	29 bp	mrna	linear	EST 10-OCT-2003					
/sub_species="morsitans"	29 bp	mrna	linear	EST 10-OCT-2003					
/db_xref="taxon:37546"	29 bp	mrna	linear	EST 10-OCT-2003					

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 29)

Lehane, M.J., Aksoy, S., Gibson, W., Kerkhoun, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

1. .29

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

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/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;

Best Local Similarity 95.2%; Pred. No. 5.4e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTT 4482

DB 9 AGTTTTTCTTTTCTTTTCTTTT 29

RESULT 637

EX554178

LOCUS

DEFINITION

Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse13h04_plc, mRNA sequence.

ACCESSION

EX554178

VERSION

EX554178.1

KEYWORDS

EST.

SOURCE

Glossina morsitans morsitans

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 29)

Lehane, M.J., Aksoy, S., Gibson, W., Kerkhoun, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

1. .29

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse13h04_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;

Best Local Similarity 95.2%; Pred. No. 5.4e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTT 4482

DB 9 AGTTTTTCTTTTCTTTTCTTTT 29

RESULT 638

EX554562

LOCUS

DEFINITION

Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse16b01_plc, mRNA sequence.

ACCESSION

EX554562

VERSION

EX554562.1

KEYWORDS

EST.

SOURCE

Glossina morsitans morsitans

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 29)

Lehane, M.J., Aksoy, S., Gibson, W., Kerkhoun, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

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School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

1. .29

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse16b01_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"

RESULT 644					
BX556342 29 bp mRNA linear EST 10-OCT-2003					
LOCUS					
DEFINITION					
BX556342 Glossina morsitans morsitans adult infected gut Glossina					
morsitans morsitans cDNA clone Tse26e07_pic, mRNA sequence.					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Glossina morsitans morsitans					
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
Hippoboscidae; Glossinidae; Glossina.					
1 (bases 1 to 29)					
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,					
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.					
Adult midgut expressed sequence tags from the tsetse fly Glossina					
morsitans morsitans and expression analysis of putative immune					
response genes					
Genome Biol. 4 (10), R63 (2003)					
MEDLINE					
PUBMED					
14519198					
COMMENT					
Contact: Hall N					
Pathogen Sequencing Unit					
The Sanger Institute The Wellcome Trust Genome Campus					
Hinxtion, Cambridge, CB10 1SA, UK					
Request for clones, please contact: Mike Lehane					
Prof. M.J.Lehane					
School of Biological Sciences,					
University of Wales,					
Bangor LL57 2UW					
All clones with suffix q1c are reverse primer reads starting at 5'					
end of the cDNA all pic reads are from					
the 3' end.					
Location/Qualifiers					
1..29					
/organism="Glossina morsitans morsitans"					
/mol_type="mRNA"					
/sub_species="morsitans"					
/db_xref="taxon:37546"					
/clone="Tse26e07_pic"					
/tissue_type="adult infected gut"					
/clone_lib="Glossina morsitans morsitans adult infected					
gut"					
/note="country: Zimbabwe; EST from adult gut infected with					
T.brucei"					
Query Match 0.3%; Score 19.4; DB 1; Length 29;					
Best Local Similarity 95.2%; Pred.No.5.4e+02;					
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY 4462 ACATTTTTTTTTTTTTTTTT 4482					
Db 9 AGTTTTTTTTTTTTTTTTTT 29					
RESULT 645					
BX556455					
LOCUS					
DEFINITION					
BX556455 Glossina morsitans morsitans adult infected gut Glossina					
morsitans morsitans cDNA clone Tse27b11_pic, mRNA sequence.					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
Glossina morsitans morsitans					
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;					
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;					
Hippoboscidae; Glossinidae; Glossina.					
1 (bases 1 to 29)					
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,					
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.					
Adult midgut expressed sequence tags from the tsetse fly Glossina					
TITLE					

```

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
        /db_xref="taxon:37546"
        /clone="Tse27e07_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected
        gut"
        /note="country: Zimbabwe; EST from adult gut infected with
        T.brucei"

    Query Match          0.3%; Score 19.4; DB 1; Length 29;
    Best Local Similarity 95.2%; Pred. No. 5.4e+02;
    Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 647
BX556517
LOCUS
DEFINITION BX556517 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse27f12_plc, mRNA sequence.
ACCESSION BX556517
VERSION
KEYWORDS
SOURCE
ORGANISM
  Glossina morsitans morsitans
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Hippoboscoidae; Glossiniidae; Glossina.
  1 (bases 1 to 29)
REFERENCE
  Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
  Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
  Adult midgut expressed sequence tags from the tsetse fly Glossina
  morsitans morsitans and expression analysis of putative immune
  response genes
  Genome Biol. 4 (10), R63 (2003)
  22881942
  PUBLISHED 14519198
  COMMENT
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J. Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
    All clones with suffix q1c are reverse primer reads starting at 5',
    end of the cDNA all plc reads are from
    the 3' end.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
        /db_xref="taxon:37546"
        /clone="Tse27f12_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected
        gut"
        /note="country: Zimbabwe; EST from adult gut infected with
        T.brucei"

    Query Match          0.3%; Score 19.4; DB 1; Length 29;
    Best Local Similarity 95.2%; Pred. No. 5.4e+02;
    Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 647
BX556517
LOCUS
DEFINITION BX556517 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse27f12_plc, mRNA sequence.
ACCESSION BX556517
VERSION
KEYWORDS
SOURCE
ORGANISM
  Glossina morsitans morsitans
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Hippoboscoidae; Glossiniidae; Glossina.
  1 (bases 1 to 29)
REFERENCE
  Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
  Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
  Adult midgut expressed sequence tags from the tsetse fly Glossina
  morsitans morsitans and expression analysis of putative immune
  response genes
  Genome Biol. 4 (10), R63 (2003)
  22881942
  PUBLISHED 14519198
  COMMENT
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J. Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
    All clones with suffix q1c are reverse primer reads starting at 5',
    end of the cDNA all plc reads are from
    the 3' end.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
        /db_xref="taxon:37546"
        /clone="Tse27f12_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected
        gut"
        /note="country: Zimbabwe; EST from adult gut infected with
        T.brucei"

    Query Match          0.3%; Score 19.4; DB 1; Length 29;
    Best Local Similarity 95.2%; Pred. No. 5.4e+02;
    Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 648
BX556670
LOCUS
DEFINITION BX556670 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse28g01_plc, mRNA sequence.
ACCESSION BX556670
VERSION
KEYWORDS
SOURCE
ORGANISM
  Glossina morsitans morsitans
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
  Hippoboscoidae; Glossiniidae; Glossina.
  1 (bases 1 to 29)
REFERENCE
  Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
  Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
  Adult midgut expressed sequence tags from the tsetse fly Glossina
  morsitans morsitans and expression analysis of putative immune
  response genes
  Genome Biol. 4 (10), R63 (2003)
  22881942
  PUBLISHED 14519198
  COMMENT
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J. Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
    All clones with suffix q1c are reverse primer reads starting at 5',
    end of the cDNA all plc reads are from
    the 3' end.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
        /db_xref="taxon:37546"
        /clone="Tse28g01_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected
        gut"
        /note="country: Zimbabwe; EST from adult gut infected with
        T.brucei"

    Query Match          0.3%; Score 19.4; DB 1; Length 29;
    Best Local Similarity 95.2%; Pred. No. 5.4e+02;
    Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 649
BX557474
LOCUS
DEFINITION BX557474 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse32f03_plc, mRNA sequence.
ACCESSION BX557474
VERSION
KEYWORDS
SOURCE
ORGANISM
  Glossina morsitans morsitans
  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

```



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Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 652
BX557758
LOCUS
DEFINITION
BX557758 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse34e06_plc, mRNA sequence.
ACCESSION
BX557758
VERSION
BX557758.1 GI:33428933
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 654
BX558583
LOCUS
DEFINITION
BX558583 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse39e03_plc, mRNA sequence.
ACCESSION
BX558583
VERSION
BX558583.1 GI:33365424
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
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Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit

```

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University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source

Location/Qualifiers

1. .29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse39e03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482

Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 655

BX562299

LOCUS

DEFINITION BX562299 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse3h07_plc, mRNA sequence.

ACCESSION

BX562299

VERSION

BX562299.1

KEYWORDS

EST.

SOURCE

ORGANISM

Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidea; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
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Genome Biol. 4 (10), R63 (2003)

MEDLINE

22881942

PUBMED

14519198

COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source

Location/Qualifiers

1. .29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse5h07_plc"

/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482

Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 656

BX563480

LOCUS

DEFINITION BX563480 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse67b04_plc, mRNA sequence.

ACCESSION

BX563480

VERSION

BX563480.1

KEYWORDS

EST.

SOURCE

ORGANISM

Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidea; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

MEDLINE

22881942

PUBMED

14519198

COMMENT

Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source

Location/Qualifiers

1. .29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse67b04_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482

Db 9 AGTTTTTTTTTTTTTTTTTT 29

RESULT 657

CF336137


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LOCUS       CF336137              29 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION  JMT--06-B10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-B10, mRNA sequence.
ACCESSION   CF336137
VERSION     CF336137.1    GI:33820654
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 29)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES             source
     1..29
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="AtJMT-overexpressing transgenic rice plasmid
            cDNA library (JMT)"
     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
            was reverse transcribed and then used for PCR. mRNA was
            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 79.3%; Pred. No. 5.4e+02;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  4457 CATGACACTTTTTTTTTTTTTTTTTTTTGT 4485
Db  1 CATGACAGTGTGTGTGTGTGTGTGTGTGTGT 29

RESULT 658
LOCUS     AW247159              24 bp    mRNA    linear    EST 07-JAN-2000
DEFINITION  2819627.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
            mRNA sequence.
ACCESSION   AW247159
VERSION     AW247159.1    GI:6590152
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 24)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other ESTs: 2819627.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:

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www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center. Vector
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 24
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LNCM2 row: B column: 12
High quality sequence stop: 24.
Location/Qualifiers
     1..24
     /organism="Homo sapiens"
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     /db_xref="taxon:9606"
     /clone="IMAGE:2819627"
     /tissue_type="small cell carcinoma"
     /cell_line="MGC3"
     /lab_host="DH10B (phage-resistant)"
     /clone_lib="NIH_MGC_7"
     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  4464 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 4487
Db  1 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 659
LOCUS     CF281313              24 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION  14ETL--08-F05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--08-F05, mRNA sequence.
ACCESSION   CF281313
VERSION     CF281313.1    GI:33658700
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES             source
     1..24
     /organism="Oryza sativa"
     /mol_type="mRNA"
     /cultivar="Nackdong"
     /db_xref="taxon:4530"

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/clone="14ETL--08-F05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTCT 4487
      |||||
DB 1 TTTTCTTTTCTTTTCTTCTT 24

RESULT 660
AZ458112
LOCUS          24 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION    IM0261E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0261E24 R, genomic survey sequence.
ACCESSION     AZ458112
VERSION       AZ458112.1 GI:10616237
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 24)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0261 row: E column: 24
Seq primer: CACACAGGACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261E24"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

/clone="14ETL--08-F05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTCT 4487
      |||||
DB 1 TTTTCTTTTCTTTTCTTCTT 24

RESULT 661
AZ486788
LOCUS          24 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION    IM0315122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315122 F, genomic survey sequence.
ACCESSION     AZ486788
VERSION       AZ486788.1 GI:10653906
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 24)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: I column: 22
Seq primer: CGTTGTAAAACGACGGCAGCT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315122"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

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inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred.No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 663	25 bp	DNA	linear	GSS 03-OCT-2000
AZ427752/c				
LOCUS				
DEFINITION				
ACCESION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

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Insert Length: 10000 Std Error: 0.00
Email: dunn@genetics.ucan.edu
Plate: 0209 row: N column: 21
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. ..25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0209N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

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/db xref="taxon:161934"
/clone="024-014-B24"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPI2-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 669
LOCUS CB174047 19 bp mRNA linear EST 09-OCT-2003
DEFINITION OR 2632F05 010529.y1 Adult mouse olfactory epithelium library Mus
VERSION Mus musculus cDNA clone 2632F05 5', mRNA sequence.
KEYWORDS EST.
SOURCE CB174047.1 GI:37592676
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Young,J.M., Shykind,B.M., Lane,R.P., Tonnes-Priddy,L., Rose,J.A.,
Walker,M., Williams,E.M. and Trask,B.J.
TITLE Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and
unequal expression levels
JOURNAL Genome Biol. 4 (11), R71.1-R71.15 (2003)
COMMENT Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org
Seq primer: M13 Reverse.

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2632F05"
/tissue_type="Adult"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/notes="Organ: Olfactory turbinates; Vector:
LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Vosshall. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 670
LOCUS CF279008 19 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--05-Cl3.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
VERSION Oryza sativa cDNA clone 14ETL--05-Cl3, mRNA sequence.
KEYWORDS EST.
SOURCE CF279008.1 GI:33656394
ORGANISM Oryza sativa

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..19
/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--05-Cl3"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH108"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 671
LOCUS CF291089 19 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-G03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
VERSION Oryza sativa cDNA clone 14ROOT--01-G03, mRNA sequence.
KEYWORDS EST.
SOURCE CF291089.1 GI:33660122
ORGANISM Oryza sativa

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)

```


JOURNAL
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source

1. .19
Location/Qualifiers
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTT 4482
Db 1 TTTT...TTTTTTT 19

RESULT 675

CF302327
LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-L24, mRNA sequence.

ACCESSION CF302327
VERSION
KEYWORDS
SOURCE EST.
GI:33674088

ORGANISM
Oryza sativa

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
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1. .19
Location/Qualifiers
/organism="Oryza sativa"
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/clone="7LEAF--07-L24"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTT 4482
Db 1 TTTT...TTTTTTT 19

RESULT 676

CF302456
LOCUS 19 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-P22, mRNA sequence.

ACCESSION CF302456
VERSION
KEYWORDS
SOURCE EST.
GI:33674217

ORGANISM
Oryza sativa

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source

1. .19
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-P22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT...TTTTTTT 19

RESULT 677

CF304589
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DEFINITION ABF1--05-G10.g1 ABF3-overexpressing transgenic rice lambda phage
cDNA library (ABF1) Oryza sativa cDNA clone ABF1--05-G10, mRNA
sequence.

ACCESSION CF304589
VERSION
KEYWORDS
SOURCE EST.
GI:33676350

ORGANISM
Oryza sativa

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,


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library (ABF) Oryza sativa cDNA clone ABF--06-L18, mRNA sequence.
ACCESSION      CF311496
VERSION        CF311496.1  GI:33683257
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SOURCE
ORGANISM       Oryza sativa
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               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1  (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

Query Match      0.3%; Score 19; DB 1; Length 19;
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RESULT 681
CF311513
LOCUS
DEFINITION  ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
               library (ABF) Oryza sativa cDNA clone ABF--06-M03, mRNA sequence.
ACCESSION      CF311513
VERSION        CF311513.1  GI:33683274
KEYWORDS
SOURCE
ORGANISM       Oryza sativa
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               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1  (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match      0.3%; Score 19; DB 1; Length 19;
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RESULT 681
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LOCUS
DEFINITION  ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
               library (ABF) Oryza sativa cDNA clone ABF--06-M03, mRNA sequence.
ACCESSION      CF311513
VERSION        CF311513.1  GI:33683274
KEYWORDS
SOURCE
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1  (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
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               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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                     then used for PCR. mRNA was prepared from ABA-responsive
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                     line."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
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RESULT 682
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LOCUS
DEFINITION  ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION      CF312403
VERSION        CF312403.1  GI:33684164
KEYWORDS
SOURCE
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1  (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     element binding transcription factor 3 overexpression
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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 682
CF312403/C
LOCUS
DEFINITION  ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
               library (ABF) Oryza sativa cDNA clone ABF--08-C07, mRNA sequence.
ACCESSION      CF312403
VERSION        CF312403.1  GI:33684164
KEYWORDS
SOURCE
ORGANISM       Oryza sativa
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1  (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
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               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY      4464 TTTT TTTT TTTT TTTT TTTT 4482
Db      19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 683
CF315299
LOCUS   HD--04-C17, g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION
ACCESSION CF315299
VERSION   1
KEYWORDS  1 (bases 1 to 19)
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
           Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Gyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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line."

QY      4464 TTTT TTTT TTTT TTTT TTTT 4482
Db      1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 684
CF316480
LOCUS   HD--05-M14, g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION
ACCESSION CF316480
VERSION   1
KEYWORDS  1 (bases 1 to 19)
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
           Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Gyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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line."

Query Match      0.3%; Score 19; DB 1; Length 19;
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RESULT 685
CF318788/c
LOCUS   HD--09-A23, b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION
ACCESSION CF318788
VERSION   1
KEYWORDS  1 (bases 1 to 19)
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS   Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
           Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Gyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
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FEATURES
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cDNA library (HD)"
/notes=vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION NACL--05-I09.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-I09, mRNA sequence.
ACCESSION CF329986
VERSION CF329986.1 GI:33808194
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RESULT 688
CF333507/c
LOCUS CF333507 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-G23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-G23, mRNA sequence.
ACCESSION CF333507
VERSION CF333507.1 GI:33815309
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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RESULT 687
CF332063
LOCUS CF332063 19 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-G19, mRNA sequence.
ACCESSION CF332063
VERSION CF332063.1 GI:33812347
KEYWORDS EST.

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SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 688
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LOCUS CF333507 19 bp mRNA linear EST 18-AUG-2003
DEFINITION JMT--02-G23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-G23, mRNA sequence.
ACCESSION CF333507
VERSION CF333507.1 GI:33815309
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--08-G23"

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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dddn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Seq: 0008 row: H column: 20
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19

FEATURES
source

1. 19
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); Was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 [gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: K column: 17
Seq primer: CACACAGGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The ligated DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (G14732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1). The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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RESULT 695
AZ340311
LOCUS
DEFINITION
19 bp DNA linear GSS 29-SEP-2000
1M0072H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
Clone UUGC1M0072H15 F, genomic survey sequence.
AZ340311
AZ340311.1 GI:10415441
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00


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Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTTTTTTTT 4482
DB 19 TTTTTCCTTTTTTTTTTTT 1

RESULT 698
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LOCUS
DEFINITION
1M0112A07R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0112A07 R, genomic survey sequence.
ACCESSION
AZ365696
VERSION
AZ365696.1 GI:10479396
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: A column: 07
Seq primer: CACACGAAACAGCTATGCC
Class: plasmid ends
High quality sequence stop: 19.

Class: plasmid ends
High quality sequence stop: 19.
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/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTTTTTTTT 4482
DB 19 TTTTTCCTTTTTTTTTTTT 1

RESULT 698
AZ365696/c
LOCUS
DEFINITION
1M0112A07R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUGC1M0112A07 R, genomic survey sequence.
ACCESSION
AZ365696
VERSION
AZ365696.1 GI:10479396
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0112 row: A column: 07
Seq primer: CACACGAAACAGCTATGCC
Class: plasmid ends
High quality sequence stop: 19.

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/db_xref="taxon:10090"
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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy

4464 TTTTTTTTTTTTTTTTTT 4482
TTTTTTTTTTTTTTTTTTTT

pb

19 TTTTTTTTTTTTTTTTTT 1
TTTTTTTTTTTTTTTTTTTT

RESULT	703
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LOCUS	
DEFINITION	AZ410050 19 bp DNA linear GSS 03-OCT-2000 IM0182P04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0182P04 F, genomic survey sequence.

ACCESSION AZ410050
 VERSION AZ410050.1 GI:10534063
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)

COMMENTS: Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0182 row: P column: 04
Seq primer: CGTTGTAAACGACGCCAGT

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High quality sequence stop: 19.
Location/Qualifiers
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/organism="Mus musculus"
/mol type="genomic DNA"
FEATURES
source
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes=Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
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 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 708
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 LOCUS
 DEFINITION
 1M0236C13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0236C13 F, genomic survey sequence.

ACCESSION
 AZ442365
 VERSION
 AZ442365.1 GI:10566378
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
 1 (bases 1 to 19)

AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D. Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0236 row: C column: 13

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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 /clone="UUGC1M0236C13"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"
 /notes=Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 709

AZ453930

LOCUS

DEFINITION
 1M0255G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0255G11 R, genomic survey sequence.

ACCESSION
 AZ453930

VERSION
 AZ453930.1 GI:10612055

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D. Weiss,R.

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT
 Contact: Robert B. Weiss

University of Utah

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0255 row: G column: 11

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"

musculus C57BL/6J (male) was obtained from the Jackson Laboratory mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1.473214[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to the adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4482
Db 19 TTTTTTTTTTTTTTTTTT 1

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RESULT 711	
LOCUS	AZ471494
DEFINITION	mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286E11 F, genomic survey sequence.
ACCESSION	AZ471494
VERSION	AZ471494.1
KEYWORDS	GI:10629619
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhauser,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss

```

University of Utah
Rm. 308, Biomedical Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0286 row: E column: 11
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="UUGCIM0286E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```

Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 [gi|4732114|gb|AF19072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.3%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
Matches 19;	Conservative	0;	Mismatches 0;	Indels 0;
QY	4464	TTTTTTTTTTTTTTTTTTTT	4482	
Db	1	TTTTTTTTTTTTTTTTTTTT	19	

RESULT	712
AZ476576	
LOCUS	19 bp DNA linear GSS 04-OCT-2000
DEFINITION	I0295F04R Mouse 10 kb plasmid UGCGIM library Mus musculus genomic clone UGCGIM0295F04 R, genomic survey sequence.
ACCESSION	AZ476576
VERSION	AZ476576.1
KEYWORDS	GI:10634701
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss

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FEATURES
    source
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                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1m library"
                /notes="vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* Xli10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4482
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Db 1 TTTTTTTTTTTTTTTTTT 19
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RESULT	713
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DEFINITION	AZ486786 1M0315D21F Mouse 10kb plasmid UUGCLIM library Mus musculus genomic clone UUGCLIM0315D21 F, genomic survey sequence.
ACCESSION	AZ486786
VERSION	AZ486786
KEYWORDS	GSS.
SOURCE	AZ486786..1 GI:10653902
ORGANISM	Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center

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FEATURES
    source
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    /organism="Mus musculus"
    /mol_type="genomic DNA"
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    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="Vector: PMD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The f

```

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4482
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Db 1 TTTTTTTTTTTTTTTTTT 19
      |||||

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RESULT 715	AZ508040/c	LOCUS	AZ508040	19 bp	DNA	linear	GSS 05-OCT-2000
DEFINITION	1M0350B04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0350B04 F, genomic survey sequence.						

VERSION	AZ508040.1	GI:10689356
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 19)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0350 row: B column: 04
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nb; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

```


adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gil4732114[gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%      Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4482
Db 19 TTTTTTTTTTTTTTTTTT 1

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RESULT	719
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LOCUS	19 bp DNA linear GSS 13-DEC-2000
DEFINITION	Musculus musculus genomic clone UUGC1M library Mus musculus genomic survey sequence.
ACCESSION	AZ593210
VERSION	AZ593210.1
KEYWORDS	GI:11715400
SOURCE	GSS:
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.: Weiss,R. 10kb plasmid whole genome scaffolding with paired end reads from 10kb plasmid inserts
TITLE	Unpublished (2000)
JOURNAL	Contact: Robert B. Weiss
COMMENT	

Pm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0404 row: C column: 09
 Seq primer: CACACAGGNAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 source

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```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 [g1473211|jb|AR159072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 4464 TTTTTTTTTTTTTTTTTTTTTT 4482
Db 19 TTTTTTTTTTTTTTTTTTTTTT 1

RESULT	720
AZ616154	
LOCUS	AZ616154
DEFINITION	Musculus musculus genomic clone UGUC1M0445P16 R, genomic survey sequence.
ACCESSION	AZ616154
VERSION	AZ616154.1
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;

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FEATURES
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  Location/Qualifiers
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    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydronamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

```

electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1|], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* Xli10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	4464	4482
pp	1	19

RESULT	721	AZ6227844	19 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	AZ627844	1M0474J05F	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION		clone UUGC1M0474J05 F, genomic survey sequence.				
ACCESSION		AZ627844				
VERSION		AZ627844.1	GI:11750130			
KEYWORDS		GSS.				
SOURCE		Mus musculus	(house mouse)			
ORGANISM		Mus musculus				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				

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FEATURES
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Location/Qualifiers
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
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 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 722
 AZ631701/c
 LOCUS
 DEFINITION 19 bp DNA linear GSS 13-DEC-2000
 clone UUGC1M0486E01 F, genomic survey sequence.
 ACCESSION
 VERSION AZ631701.1 GI:11753891
 KEYWORDS
 SOURCE GSS.
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingley, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0486 row: E column: 01
 Seq primer: CGTTGTAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

FEATURES
 source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0486E01"
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 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
 |||||
 DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 723
 AZ633821/c
 LOCUS
 DEFINITION 19 bp DNA linear GSS 13-DEC-2000
 clone UUGC1M0489H15 F, genomic survey sequence.
 ACCESSION
 VERSION AZ633821.1 GI:11756011
 KEYWORDS
 SOURCE GSS.
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Stokes, R., Tingley, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

FEATURES
 source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /clone="UUGC1M0489H15"
 /sex="Male"
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 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated

Adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732141|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to the adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells.

and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 728
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LOCUS
DEFINITION
1M056H03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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ACCESSION
AZ764497
VERSION
AZ764497.1 GI:12879521
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: H column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
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Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
|||||
Db 19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 729
AZ764522/c
LOCUS
DEFINITION
1M0560E16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560E16 R, genomic survey sequence.
ACCESSION
AZ764522
VERSION
AZ764522.1 GI:12879571
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 19)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: E column: 16
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

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Matches   19; Conservative    0; Mismatches    0; Indels      0; Gaps       0;
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Qy        4464 TTTTTTTTTTTTTTTT 4482  
          |||  
Db        19  TTTTTTTTTTTTTTTT 1
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RESULT 732
AZ77858/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AZ77858 19 bp DNA linear GSS 16-FEB-2001
2M0014020F Mouse 10kb plasmid UGCG1M library Mus musculus genomic
clone UGCG2M0014020 F, genomic survey sequence.
A277858
A277858.1 GI:12908925
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rother,K., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0014 row: 0 column: 20
Seq primer: CGTTGTAACAGCGGCAGT
Class: plasmid ends
High quality sequence stop: 19.

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/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptorated DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptorated mouse DNA was annealed to
adaptorated vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 733	
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LOCUS	19 bp DNA linear GSS 16-FEB-2001
DEFINITION	2M0016E16R Mouse 10kb plasmid UGCM1 library Mus musculus genomic clone UGUC2M0016E16 R, genomic survey sequence.
ACCESSION	AZ779901
VERSION	AZ779901.1
KEYWORDS	GI:12911024
SOURCE	GSS.
ORGANISM	Mus musculus (house mouse)
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0016 row: E column: 16 Seq primer: CACACGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.

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FEATURES
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (Gi|14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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Query Match	0.3%	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
Matches 19; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 734
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LOCUS
DEFINITION
  19 bp DNA linear GSS 16-FEB-2001
  2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0021003 R, genomic survey sequence.
ACCESSION
  AZ781876
VERSION
  AZ781876.1 GI:12915007
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0021 row: 0 column: 03
  Seq primer: CACACGAGAAACGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 19.
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    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 735
AZ787634
LOCUS
DEFINITION
  19 bp DNA linear GSS 16-FEB-2001
  2M0034M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC2M0034M12 F, genomic survey sequence.
ACCESSION
  AZ787634
VERSION
  AZ787634.1 GI:12926621
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 19)
REFERENCE
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0034 row: M column: 12
  Seq primer: CGTGTAAACGACGCGCAGT
  Class: plasmid ends
  High quality sequence stop: 19.
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  1..19
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    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adapted DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adapted mouse DNA was annealed to
    adapted vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTT TTTT TTTT TTTT TTTT 4482
DB 19 TTTT TTTT TTTT TTTT TTTT 1

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Db	1	TTTTTTTTTTTTTTTTTTT	19
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DEFINITION	clone UUGC2M0034124 R, genomic survey sequence.		
ACCESSION	AZ788058		
VERSION	AZ788058.1	GI:12927475	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 19)		
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0034 row: 1 column: 24 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.		
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	/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	0.3%;	Score 19;	DB 1; Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;	
Matches	19;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	4464	TTTTTTTTTTTTTTTTTTT	4482
Db	1	TTTTTTTTTTTTTTTTTTT	19

RESULT 737	AZ789590		
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DEFINITION	clone UUGC2M0037G06 R, genomic survey sequence.		
ACCESSION	AZ789590		
VERSION	AZ789590.1	GI:12930573	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 19)		
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0037 row: G column: 06 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 19.		
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	/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."		
Query Match	0.3%;	Score 19;	DB 1; Length 19;
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Matches	19;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
Qy	4464	TTTTTTTTTTTTTTTTTTT	4482
Db	1	TTTTTTTTTTTTTTTTTTT	19


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ACCESSION     AZ801970
VERSION       AZ801970
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT       Unpublished (2000)
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0060 row: I column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
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/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4482
Db 1 TTTTTTTTTTTTTTTTTT 19

AZ822225      AZ822225      19 bp      DNA      linear      GSS 20-FEB-2001
LOCUS
DEFINITION    2M0095E17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0095E17 F, genomic survey sequence.
ACCESSION     AZ822225
VERSION       AZ822225
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: E column: 17
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
source
1. .19
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0095E17"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4482
Db 1 TTTTTTTTTTTTTTTTTT 19

AZ841581      AZ841581      19 bp      DNA      linear      GSS 20-FEB-2001
LOCUS
DEFINITION    2M0095E17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0095E17 F, genomic survey sequence.
ACCESSION     AZ841581/c
VERSION       AZ841581/c
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT       Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0095 row: E column: 17
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES
source
1. .19
/organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M0095E17"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTT 4482
Db 1 TTTTTTTTTTTTTTTTTT 19

RESULT 741
AZ822225

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clone UUGC2M0139A16 R, genomic survey sequence.
AZ841622
VERSION
AZ841622.1 GI:13011530
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0139 row: A column: 16
Seq primer: CACACAGGACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0139A16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1m library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnarses/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

```

Query Match          0.3%      Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    4464 TTTTTTTTTTTTTTTT 4482
      ||| ||||| ||||| |||||
Db     19 TTTTTTTTTTTTTTTT 1

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AZ861896 19 bp DNA linear GSS 21-FEB-2001
 ZM0168P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0168P10 R, genomic survey sequence.
 DEFINITION
 LOCUS

```

ACCESSION      AZ861896
VERSION        AZ861896.1  GI:13058674
KEYWORDS
SOURCE         Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT        Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0168 row: P column: 10
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0168P10"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
              Query Match      0.3%; Score 19; DB 1; Length 19;
              Best Local Similarity 100.0%; Pred. No. 2.4e+02;
              Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
          |||||
Db  19    TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 745
AZ936798/c
LOCUS
DEFINITION  AZ936798 19 bp DNA linear GSS 26-APR-2001
            2M0193L10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0193L10 R, genomic survey sequence.
ACCESSION  AZ936798

```

```

AZ936798.1  GI:13795379
GSS.
Mus musculus (house mouse)
Mus musculus
REFERENCE
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL
COMMENT        Unpublished (2000)
              Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0193 row: L column: 10
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC2M0193L10"
                /sex="Female"
                /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC2M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (female) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
              Query Match      0.3%; Score 19; DB 1; Length 19;
              Best Local Similarity 100.0%; Pred. No. 2.4e+02;
              Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
          |||||
Db  19    TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 746
AZ985501/c
LOCUS
DEFINITION  AZ985501 19 bp DNA linear GSS 27-APR-2001
            2M0267E21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0267E21 F, genomic survey sequence.
ACCESSION  AZ985501
VERSION     AZ985501.1  GI:13856728

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KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0267 row: E column: 21
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0267E21"
            /sex="Female"
            /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC2M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (female) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      |||||
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 747
BH000498/c      19 bp DNA linear GSS 27-APR-2001
LOCUS           2M0288121F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION      clone UUGC2M0288121 F, genomic survey sequence.
ACCESSION       BH000498
VERSION         BH000498.1 GI:13871724
KEYWORDS        GSS.

```

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SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0288 row: I column: 21
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES
source      1..19
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0288121"
            /sex="Female"
            /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC2M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (female) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      |||||
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 748
AL587572        20 bp mRNA linear EST 02-MAR-2001
LOCUS           AL587572 BP Chicken Brain Library Gallus gallus cdna clone
DEFINITION      ROS0599B11, mRNA sequence.
ACCESSION       AL587572
VERSION         AL587572.1 GI:13192606
KEYWORDS        EST.
SOURCE          Gallus gallus (chicken)

```

```

ORGANISM      Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS      Murray,F.
TITLE        BP Chicken Brain Library
JOURNAL      Unpublished (2001)
COMMENT      Dept. Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UK
              Tel: +44 (0)131 527 4200
              Fax: +44 (0)131 440 0434
              Email: frazer.murray@bbsrc.ac.uk
              GCGGCCGCTTTTGTG 4484
              (*6854-
              Seq primer: M13F.
              Location/Qualifiers
                1. .20
                  /organism="Gallus gallus"
                  /mol_type="mRNA"
                  /db_xref="taxon:9031"
                  /clone="ROS05B11"
                  /tissue_type="Brain"
                  /dev_stage="Unknown"
                  /lab_host="DH10B"
                  /clone_lib="BP Chicken Brain Library"
                  /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
                  unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
                  5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
                  GCGGCCGCTTTTGTG 4484
                  Clonetechn (*6854-1)"

FEATURES
source
Query Match      0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4466  TTTTGTG 4484
            |||||||
Db      2  TTTTGTG 20

RESULT 749
LOCUS      AL587727
DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  AL587727.1 GI:13192761
VERSION     AL587727
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS      Murray,F.
TITLE        BP Chicken Brain Library
JOURNAL      Unpublished (2001)
COMMENT      Dept. Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UK
              Tel: +44 (0)131 527 4200
              Fax: +44 (0)131 440 0434
              Email: frazer.murray@bbsrc.ac.uk
              GCGGCCGCTTTTGTG 4484
              (*6854-
              Seq primer: M13F.
              Location/Qualifiers
                1. .20
                  /organism="Gallus gallus"

Query Match      0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4466  TTTTGTG 4484
            |||||||
Db      1  TTTTGTG 19

RESULT 749
LOCUS      AL587727
DEFINITION AL587727 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  AL587727.1 GI:13192761
VERSION     AL587727
KEYWORDS   EST.
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS      Murray,F.
TITLE        BP Chicken Brain Library
JOURNAL      Unpublished (2001)
COMMENT      Dept. Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UK
              Tel: +44 (0)131 527 4200
              Fax: +44 (0)131 440 0434
              Email: frazer.murray@bbsrc.ac.uk
              GCGGCCGCTTTTGTG 4484
              (*6854-
              Seq primer: M13F.
              Location/Qualifiers
                1. .20
                  /organism="Gallus gallus"

Query Match      0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4466  TTTTGTG 4484
            |||||||
Db      2  TTTTGTG 20

RESULT 750
LOCUS      CF282002
DEFINITION CF282002 14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION  CF282002.1 GI:33659389
VERSION     CF282002
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              Unpublished (2003)
              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
              Location/Qualifiers
                1. .20
                  /organism="Oryza sativa"
                  /mol_type="mRNA"
                  /cultivar="Nackdong"
                  /db_xref="taxon:4530"
                  /clone="14ETL--09-F01"
                  /tissue_type="leaf"
                  /dev_stage="14 days after germination"
                  /lab_host="E.coli DH10B"
                  /clone_lib="Rice etiolated leaf plasmid cDNA library
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                  /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                  with oligoribonucleotides and then used as templates for
                  RT-PCR."

Query Match      0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4466  TTTTGTG 4484
            |||||||
Db      2  TTTTGTG 20

RESULT 751

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4482
Db 1 TTTT... 19

RESULT 756
A2638704/c
LOCUS
DEFINITION
clone UUGC1M0498E13 R, genomic survey sequence.

ACCESSION
A2638704
VERSION
A2638704.1 GI:11760894
KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: E column: 13

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0498E13"
/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4482
Db 20 TTTT... 2

RESULT 757

A2821905/c

LOCUS

DEFINITION
2M0094D20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0094D20 R, genomic survey sequence.

ACCESSION
A2821905

VERSION
A2821905.1 GI:12991813

KEYWORDS
GSS.

SOURCE
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)

REFERENCE

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT
Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: D column: 20

Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0094D20"
/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4466 TTTT...TTTGTG 4484
Db      20 TTTT...TTTTTTT 2

RESULT 758
AZ858419/c
LOCUS      20 bp      DNA      linear      GSS 21-FEB-2001
DEFINITION      2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION      AZ858419
VERSION      AZ858419.1 GI:13051545
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weisse,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: dunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0163 row: 0 column: 03
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
FEATURES      source
              Location/Qualifiers
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                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
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                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: pWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [gi4732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      0.3%; Score 19; DB 1; Length 20;
              Best Local Similarity 100.0%; Pred. No. 2.7e+02;
              Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTT...TTTTTTT 4482
Db      20 TTTT...TTTTTTT 2

RESULT 758
AZ858419/c
LOCUS      20 bp      DNA      linear      GSS 21-FEB-2001
DEFINITION      2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION      AZ858419
VERSION      AZ858419.1 GI:13051545
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D., Weisse,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: dunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0163 row: 0 column: 03
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 20.
FEATURES      source
              Location/Qualifiers
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                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /strain="C57BL/6J"
                  /db_xref="taxon:10090"
                  /clone="UUGC2M0163003"
                  /sex="Male"
                  /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                  /note="Vector: pWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 [gi4732114|gb|AF129072.1], a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      0.3%; Score 19; DB 1; Length 20;
              Best Local Similarity 100.0%; Pred. No. 2.7e+02;
              Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTT...TTTTTTT 4482
Db      20 TTTT...TTTTTTT 2

RESULT 759
AL587702
LOCUS      21 bp      mRNA      linear      EST 02-MAR-2001
DEFINITION      BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION      AL587702
VERSION      AL587702.1 GI:13192736
KEYWORDS      EST.
SOURCE      Gallus gallus (chicken)
ORGANISM      Gallus gallus
REFERENCE      1 (bases 1 to 21)
AUTHORS      Murray,F.
TITLE      BP Chicken Brain Library
JOURNAL      Unpublished (2001)
COMMENT      Contact: Frazer Murray
              Dept. Genomics and Bioinformatics
              Roslin Institute
              Roslin, Midlothian, EH25 9PS, UK
              Tel: +44 (0)131 527 4200
              Fax: +44 (0)131 440 0434
              Email: frazer.murray@bbsrc.ac.uk
              GCGGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech
              (*6854-
              Seq primer: M13P.
              Location/Qualifiers
                1..21
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                  /dev_stage="Unknown"
                  /lab_host="DH10B"
                  /clone_lib="BP Chicken Brain Library"
                  /note="Vector: pSP0RT1; Site 1: NotI; Site 2: SalI; Cloned
              unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
              5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
              GCGGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
              Clontech (*6854-1)"
              Query Match      0.3%; Score 19; DB 1; Length 21;
              Best Local Similarity 95.0%; Pred. No. 3.1e+02;
              Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464 TTTT...TTTTTTT 4483
Db      2 TTTT...TTTTTTT 21

RESULT 760
CF302218
LOCUS      21 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--07-117.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION      CF302218
VERSION      CF302218.1 GI:33673979
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
REFERENCE      1 (bases 1 to 21)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
              Large-scale Sequencing Analysis of Rice ESTs
              TITLE      Large-scale Sequencing Analysis of Rice ESTs

```

```

JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-07-117"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
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RESULT 761
CF314260 21 bp mRNA linear EST 15-AUG-2003
LOCUS library (HD) Oryza sativa cDNA clone HD--02-L11, mRNA sequence.
DEFINITION
ACCESSION CF314260
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 21)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-C16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 22 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4

RESULT 763
AZ309907
LOCUS
DEFINITION 1M0017N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0017N14 F, genomic survey sequence.
ACCESSION AZ309907
VERSION AZ309907.1 GI:10351367
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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/lab_host="E.coli DH10B"
 /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.3%; Score 19; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482
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 Db 8 TTTT TTTT TTTT TTTT TTTT 26

RESULT 766
 TA236D08P/c
 LOCUS
 DEFINITION T. brucei sheared genomic DNA clone 236d08, forward sequence,
 genomic survey sequence.

ACCESSION AL482943
 VERSION AL482943.1 GI:11847403
 KEYWORDS GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 26)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (FRE927/4 Gutrat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).

Email: neilsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
 Location/Qualifiers

1..26
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strains="FRE927"
 /db_xref="taxon:5691"
 /clone="236d08"

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 Best Local Similarity 95.0%; Pred. No. 5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTT TTTT TTTT TTTT TTTT 4481
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 Db 20 ATT TTTT TTTT TTTT TTTT 1

RESULT 767

BI094728

LOCUS
 DEFINITION EST-CD34N-059 cDNA library of human CD 34+ stem/progenitor cells
 Homo sapiens cDNA 3', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Homo sapiens (human)

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 27)

AUTHORS Zhou, G., Chen, J., Lee, S., Terry, C., Rowley, J.D. and Wang, S.M.

TITLE The pattern of gene expression in human hematopoietic CD34+

JOURNAL stem/progenitor cells

COMMENT Unpublished (2001)

Contact: Wang SM

Hem/Onc

University of Chicago Medical Center

5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA

Tel: 773-702-6788

Fax: 773-702-3002

Email: swang@midway.uchicago.edu

This EST fragment was amplified from cDNA Library of human CD 34+
 stem/progenitor cells with GLGI technique (Generation of Longer
 cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
 Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
 the first CATG site of the targeted cDNA sequence.

Seq primer: M13 Forward.

FEATURES
 Location/Qualifiers

1..27

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="Bone marrow"

/cell_type="CD34+ stem/progenitor cells"

/clone_lib="cDNA library of human CD 34+ stem/progenitor
 cells"

/note="3' ESTs converted from the SAGE tag sequences using
 GLGI method"

Query Match 0.3%; Score 19; DB 1; Length 27;
 Best Local Similarity 81.5%; Pred. No. 5.4e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4470 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4496
 |||||
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 27

RESULT 768
 CF311022

LOCUS

DEFINITION

ABF--06-B07.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--06-B07, mRNA sequence.

ACCESSION

CF311022

VERSION

CF311022.1 GI:33682783

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
 Location/Qualifiers

1..27

source

/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCACTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH). "	
Query Match	0.3%; Score 19; DB 1; Length 27;
Best Local Similarity	100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 4464	TTTTTTTTTTTTTTTTTTT 4482
DB 1	TTTTTTTTTTTTTTTTTTT 19
RESULT 770	
TA386G03Q	27 bp DNA linear GSS 13-DEC-2000
LOCUS	T. brucei sheared genomic DNA clone 386G03, reverse sequence, genomic survey sequence.
DEFINITION	
ACCESSION	AL498287
VERSION	AL498287.1 GI:11874009
KEYWORDS	GSS.
SOURCE	Trypanosoma brucei
ORGANISM	Trypanosoma brucei
REFERENCE	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
AUTHORS	1 (bases 1 to 27) Hall, N., Bowman, S., Lennard, N. J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S. E., Rajadream, M. A. and Barrell, B. G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J. C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/ .
FEATURES	Location/Qualifiers
Source	1..27 /organism="Trypanosoma brucei" /mol_type="genomic DNA" /strain="TREU927" /db_xref="taxon:5691" /clone="j386G03"
Query Match	0.3%; Score 19; DB 1; Length 27;
Best Local Similarity	100.0%; Pred. No. 5.4e+02;
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY 4466	TTTTTTTTTTTTTTTTTTG 4484
DB 1	TTTTTTTTTTTTTTTTTTG 19

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RESULT 771
A1971979/c
LOCUS
DEFINITION
  28 bp mRNA linear EST 27-OCT-1999
  wv30h06.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:2531099 3'
  similar to TR:063545 063545 NADH DEHYDROGENASE SUBUNIT 5 ; contains
  TAB1 b1 TAR1 repetitive element ; , mRNA sequence.
ACCESSION
  A1971979
VERSION
  A1971979.1 GI:5768805
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 28)
REFERENCE
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
  R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
  Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
  I.M.A.G.E. Consortium DNA Sequencing by: Washington University
  Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
  1..28
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2531099"
  /tissue_type="fibrotheoma"
  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NCI CGAP Ov18"
  /note="Organ: ovary; Vector: p773D-Pac (Pharmacia) with a
  modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
  strand cDNA was primed with a Not I - oligo(dT) primer [5'
  TGTTACCAATCTGAAGTCGAGCGCGCGACATTTTCTTTTCTT 3'];
  double-stranded cDNA was ligated to Eco RI adaptors
  (Pharmacia), digested with Not I and cloned into the Not
  I and Eco RI sites of the modified p773 vector. Library
  went through one round of normalization, and was
  constructed by Bento Soares and M. Fatima Bonaldo. "
Query Match
  Best Local Similarity 0.3%; Score 19; DB 1; Length 28;
  Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTCT 4485
  Db 28 TGTCTTTTCTTTTCTTTTCTTTTCTTCT 2
RESULT 772
AZ803177
LOCUS
DEFINITION
  28 bp DNA linear GSS 16-FEB-2001
  2M0063K21F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
  clone UUGC2M0063K21 F, genomic survey sequence.
ACCESSION
  AZ803177
VERSION
  AZ803177.1 GI:12955500
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 28)
REFERENCE
  Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0063 row: K column: 21
  Seq primer: CGTGTAAACGACGCGCCAGT
  Class: plasmid ends
  High quality sequence stop: 28.
  Location/Qualifiers
    1..28
    /organism="Mus musculus"
    /mol_type="genomic DNA"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0063K21"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /clone_lib="Mouse 10kb plasmid UUGCLM library"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
    inducible derivative of plasmid RI. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
Query Match
  Best Local Similarity 0.3%; Score 19; DB 1; Length 28;
  Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
  Qy 6078 TTTCTTTCTCTTTTACTTGGGCGCTGG 6104
  Db 2 TTTCTTTCTCTCTCTGCGGCGCTTG 28
RESULT 773
TA173D10P/c
LOCUS
DEFINITION
  T. brucei sheared genomic DNA clone 173d10, forward sequence,
  genomic survey sequence.
ACCESSION
  AL473898
VERSION
  AL473898.1 GI:11839314
KEYWORDS
  GSS.
SOURCE
  Trypanosoma brucei
  Trypanosoma brucei
  Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  Trypanosoma.
  1 (bases 1 to 28)
REFERENCE
  Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

```


library (ABF) Oryza sativa cDNA clone ABF--05-J14, mRNA sequence.
 CF310757
 VERSION CF310757.1 GI:33682518
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 29)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..29
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="ABF-05-J14"
 /tissue_type="leaf"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 19; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4466 TTTTCTTTTCTTTTCTG 4484
 |||||
 Db 29 TTTTCTTTTCTTTTCTG 11

RESULT 777
 CF298427
 LOCUS 22 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--01-M24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-M24, mRNA sequence.
 ACCESSION CF298427
 VERSION CF298427.1 GI:33670188
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 22)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1..22
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF--01-M24"
 /tissue_type="leaf"
 /dev_stages="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 3.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4469 TTTTCTTTTCTTTTCTTGA 4490
 |||||
 Db 1 TTTTCTTTTCTTTTCTTGA 22

RESULT 778

TA303G05P/c
 LOCUS 22 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence, genomic survey sequence.
 ACCESSION AL497383
 VERSION AL497383.1 GI:11865504
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 1 (bases 1 to 22)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Direct Submision
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES

source
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="303G05"

Query Match 0.3%; Score 18.8; DB 1; Length 22;
 Best Local Similarity 90.9%; Pred. No. 3.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTGT 4485
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 Db 22 TTTTCTTTTCTTTTCTTGT 11

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RESULT 779
BX568055      23 bp mRNA linear EST 14-OCT-2003
LOCUS        morsitans morsitans adult infected gut Glossina
DEFINITION   morsitans morsitans cDNA clone Tse91f03_pic, mRNA sequence.
ACCESSION    BX568055
VERSION      BX568055.1 GI:33434952
KEYWORDS     EST.
SOURCE       Glossina morsitans morsitans
ORGANISM     Glossina morsitans morsitans
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Hippoboscidae; Glossinidae; Glossina.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
              Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE        Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J. Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all pic reads are from
              the 3' end.
FEATURES     source
              Location/Qualifiers
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                /mol_type="mRNA"
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                /db_xref="taxon:37546"
                /clone="Tse91f03_pic"
                /tissue_type="adult infected gut"
                /clone_lib="Glossina morsitans morsitans adult infected
                gut"
                /notes="country: Zimbabwe; EST from adult gut infected with
                T.brucei"
Query Match      0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTGT 4485
Db 1 TTTTTCCTTTTTCCTTTTAT 22

RESULT 780
CF290997      23 bp mRNA linear EST 14-AUG-2003
LOCUS        14ROOT--01-E03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION   sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
ACCESSION    CF290997
VERSION      CF290997.1 GI:33660030
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     source
              Location/Qualifiers
                1..23
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
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                /clone="14ROOT--01-E03"
                /tissue_type="root"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice root plasmid cDNA library (14ROOT)"
                /notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
Query Match      0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4468 TTTTTCCTTTTTCCTTTTGTCTTG 4489
Db 1 TTTTTCCTTTTTCCTTTTGGCTGG 22

RESULT 781
CF311534      23 bp mRNA linear EST 15-AUG-2003
LOCUS        ABF--06-M14.b1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
ACCESSION    CF311534
VERSION      CF311534.1 GI:33683295
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES     source
              Location/Qualifiers
                1..23
                /organism="Oryza sativa"
                /mol_type="mRNA"
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                /clone="ABF--06-M14"
                /tissue_type="leaf"
                /dev_stage="14 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="ABF3-overexpressing transgenic rice plasmid
                cDNA library (ABF)"
                /notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive

```

and selected for ampicillin resistance."

Query Match 0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 783
AZ486853
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
    source

```

```

FEATURES
source
high quantity sequence map: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUCG1W0315M14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1m library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

Query Match          0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTTTGT 4485
      ||||| ||||| ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTT 22

RESULT 784
AZ627841
LOCUS
DEFINITION
  1M0474E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0474E01 F, genomic survey sequence.
ACCESSION
  AZ627841
VERSION
  AZ627841.1 GI:11750127
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 23)
REFERENCE
  Authors
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
  Title
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0474 row: E column: 01
    Seq primer: CGTTGTAACGACGCGCCAGT
    Class: plasmid ends
    High quality sequence stop: 23.
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        /mol_type="genomic DNA"
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        /notes="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match          0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTTTGT 4485
      ||||| ||||| ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTT 22

RESULT 785
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LOCUS
DEFINITION
  1M0510O05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0510O05 R, genomic survey sequence.
ACCESSION
  AZ645254
VERSION
  AZ645254.1 GI:11774572
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 23)
REFERENCE
  Authors
    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
  Title
    Mouse whole genome scaffolding with paired end reads from 10kb
    plasmid inserts
  JOURNAL
    Unpublished (2000)
  COMMENT
    Contact: Robert B. Weiss
    University of Utah Genome Center
    University of Utah
    Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
    84112, USA
    Tel: 801 585 5606
    Fax: 801 585 7177
    Email: ddunn@genetics.utah.edu
    Insert Length: 10000 Std Error: 0.00
    Plate: 0510 row: O column: 05
    Seq primer: CACACAGGAACACGCTATGACC
    Class: plasmid ends
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        /sex="Male"
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        /notes="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

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[illegible]

Best Local Similarity 90.9%; Pred. No. 4.1e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
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Dd	1	TTTTTTTCTTTTCTTTTCTTTT 22			
RESULT 786					
TA55C06P 23 bp DNA linear GSS 13-DEC-2000					
LOCUS T. brucei sheared genomic DNA clone 55c06, forward sequence, genomic survey sequence.					
DEFINITION					
ACCESSION AL455778					
VERSION AL455778.1 GI:11856729					
KEYWORDS GSS.					
SOURCE Trypanosoma brucei					
ORGANISM Trypanosoma brucei					
Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.					
REFERENCE 1 (bases 1 to 23)					
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,M., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.					
TITLE Direct Submission					
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk					
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).					
Email: nelsayed@tigr.org					
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.					
FEATURES source					
Location/Qualifiers					
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Query Match 0.3%; Score 18.8; DB 1; Length 23; Best Local Similarity 90.9%; Pred. No. 4.1e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
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Dd	23	TTTTTTTCTTTTCTTTTCTTTT 2			
RESULT 787					
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LOCUS 2M017F23R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0177F23 R, genomic survey sequence.					
DEFINITION					
ACCESSION AZ867155					
VERSION AZ867155.1 GI:13069179					
KEYWORDS GSS.					
SOURCE Mus musculus (house mouse)					
ORGANISM Mus musculus					
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)					
REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Lehane,M.F., Lehane,S. and Hall,N.					
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0177 row: F column: 23 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 25. Location/Qualifiers					
FEATURES source					
1..25					
/organism="Mus musculus"					
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/clone="UUGC2M0177F23"					
/sex="Male"					
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGCIM library"					
/notes="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."					
Query Match 0.3%; Score 18.8; DB 1; Length 25; Best Local Similarity 90.9%; Pred. No. 4.9e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
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Dd	22	ATTATTTTCTTTTCTTTTCTTTT 1			
RESULT 788					
BX555323 27 bp mRNA linear EST 10-OCT-2003					
LOCUS BX555323 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tseig09_pic, mRNA sequence.					
DEFINITION					
ACCESSION BX555323					
VERSION BX555323.1 GI:33379323					
KEYWORDS EST.					
SOURCE Glossina morsitans morsitans					
ORGANISM Glossina morsitans morsitans					
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidea; Glossinidae; Glossina.					
REFERENCE 1 (bases 1 to 27)					
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.					

TITLE Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES source

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Location/Qualifiers
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/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 18.8; DB 1; Length 27;
Best Local Similarity 90.9%; Pred. No. 5.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 6 GGTGCTTTTTTTTTTTTTTTTTT 27
|||||

RESULT 789
TA247F06P/c
LOCUS TA247F06P 30 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 247f06, forward sequence, genomic survey sequence.
ACCESSION AL483252
VERSION AL483252.1 GI:11848928
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
1 (bases 1 to 30)
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R., Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L., Melville S.E., Rajandream M.A. and Barrell B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES source

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Db 30 AAAAAAATTTTTTTTTTTTTTTT 1
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RESULT 790
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LOCUS AA912788 25 bp mRNA linear EST 14-APR-1998
DEFINITION ol31c03.81 Soares NFL T.GBC.S1 Homo sapiens cDNA clone IMAGE:1525060 3' similar to SW:YA2C_SCHPO Q09703 HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME 1 PRECURSOR.; mRNA sequence.
ACCESSION AA912788
VERSION AA912788.1 GI:3052180
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/clone_lib="Soares NFL T.GBC.S1"
/notes="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site: 1; Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 0.2%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 5.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 25 CTTTTTCTATTTTGTGTGAT 1
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RESULT 791

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
SOURCE

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Best Local Similarity 84.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DEFINITION		clone UGCLIM0225B15	R, genomic survey	sequence.

ACCESSION AZ437459
VERSION AZ437459.1 GI:10561472
KEYWORDS GSS.

SOURCE	ORGANISM
Mus musculus (house mouse)	
Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokess, R., Tingey, A. von

1 (bases 1 to 26)

TITLE
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
Unpublished (2000)
Prasanna Insects

CONTACT: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5506
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0225 row: B column: 15
Seq primer: CACACGGAACACTTACGCC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES

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/clone="UUCG1M0225B15"  
/sex="Male"
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="vector: pWD42b; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gil4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 18.6; DB 1; Length 26;
Best Local Similarity 84.0%; Pred. No. 5.8e+02;
Matches 21: Conservative 0; Mismatches 4; Indels

QY 4463 CTTTCTTTTTTTTTTTTTTGTC 4487
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Db 2 CTTTCTCTCTCTCTCTCTCTCT 26

RESULT 800

LOCUS	AZ771474	26 bp	DNA	linear	GSS 16-FEB-2001
DEFINITION	1M0573108R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0573108 R, genomic survey sequence.				

ACCESSION AZ771474
VERSION AZ771474.1 GI:12893772
KEYWORDS GSS.

SOURCE ORGANISM	Mus musculus (house mouse)
Mus musculus	
Mus musculus	

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D. Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kbp plasmid inserts

JOURNAL
Unpublished (2000)

COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Class: plasmid ends
High quality sequence stop: 26.

FEATURES
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Location/Qualifiers
high quality sequence stop. 20.

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/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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      ||| TTTT|||||TTTTTTTTTTTTTT 28
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 806
BX549709
LOCUS BX549709 28 bp mRNA linear EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse109e05_plc, mRNA sequence.
ACCESSION BX549709
VERSION BX549709.1 GI:33368870
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse109e05_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
      ||| TTTT|||||TTTTTTTTTTTTTT 28
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 808
BX551489
LOCUS BX551489 28 bp mRNA linear EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse118h06_plc, mRNA sequence.
ACCESSION BX551489
VERSION BX551489.1 GI:33375688
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)

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Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 807
BX551130
LOCUS BX551130 28 bp mRNA linear EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse116g06_plc, mRNA sequence.
ACCESSION BX551130
VERSION BX551130.1 GI:33374984
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse116g06_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
      ||| TTTT|||||TTTTTTTTTTTTTT 28
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 808
BX551489
LOCUS BX551489 28 bp mRNA linear EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse118h06_plc, mRNA sequence.
ACCESSION BX551489
VERSION BX551489.1 GI:33375688
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)

```

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AUTHORS      Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
              Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE        Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J.Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all pic reads are from
              the 3' end.

FEATURES     source
              1. .28
              /organism="Glossina morsitans morsitans"
              /mol_type="mRNA"
              /sub_species="morsitans"
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              /clone="Tseil19a04_pic"
              /tissue_type="adult infected gut"
              /clone_lib="Glossina morsitans morsitans adult infected
              gut"
              /note="country: Zimbabwe; EST from adult gut infected with
              T.brucei"

              Query Match      0.2%; Score 18.6; DB 1; Length 28;
              Best Local Similarity 84.0%; Pred. No. 6.8e+02;
              Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY           4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db           4 TAGATAGTTTTTTTTTTTTTTTTTT 28

RESULT 810
BX551765
LOCUS
DEFINITION  BX551765 Glossina morsitans morsitans adult infected gut Glossina
              morsitans morsitans cDNA clone Tseilf03_pic, mRNA sequence.
ACCESSION   BX551765
VERSION     BX551765.1 GI:33376092
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
ORGANISM    Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
            1 (bases 1 to 28)
REFERENCE   1 (bases 1 to 28)
AUTHORS     Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE       Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL     Genome Biol. 4 (10), R63 (2003)
MEDLINE     22881942
PUBMED      14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all pic reads are from
            the 3' end.

FEATURES     source
              1. .28
              /organism="Glossina morsitans morsitans"
              /mol_type="mRNA"
              /sub_species="morsitans"
              /db_xref="taxon:37546"
              /clone="Tseilf03_pic"
              /tissue_type="adult infected gut"
              /clone_lib="Glossina morsitans morsitans adult infected
              gut"
              /note="country: Zimbabwe; EST from adult gut infected with
              T.brucei"

              Query Match      0.2%; Score 18.6; DB 1; Length 28;
              Best Local Similarity 84.0%; Pred. No. 6.8e+02;
              Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY           4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db           4 TAGATAGTTTTTTTTTTTTTTTTTT 28

RESULT 809
BX551507
LOCUS
DEFINITION  BX551507 Glossina morsitans morsitans adult infected gut Glossina
              morsitans morsitans cDNA clone Tseil19a04_pic, mRNA sequence.
ACCESSION   BX551507
VERSION     BX551507.1 GI:33375706
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
ORGANISM    Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
            1 (bases 1 to 28)
REFERENCE   1 (bases 1 to 28)
AUTHORS     Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE       Adult midgut expressed sequence tags from the tsetse fly Glossina
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            response genes
JOURNAL     Genome Biol. 4 (10), R63 (2003)
MEDLINE     22881942
PUBMED      14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW

```

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Best Local Similarity 84.0%; Pred. No. 6.8e+02; Mismatches 4; Indels 0; Gaps 0;
Matches 21; Conservative 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 811
BX551818 28 bp mRNA linear EST 10-OCT-2003
LOCUS BX551818 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tseil1h10_p1c, mRNA sequence.
ACCESSION BX551818
VERSION BX551818.1 GI:33376144
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tseil1h10_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 813
BX553072 28 bp mRNA linear EST 10-OCT-2003
LOCUS BX553072 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tseil27b06_p1c, mRNA sequence.
ACCESSION BX553072
VERSION BX553072.1 GI:33377271
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK

```

```

Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tseil21g06_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 813
BX553072 28 bp mRNA linear EST 10-OCT-2003
LOCUS BX553072 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tseil27b06_p1c, mRNA sequence.
ACCESSION BX553072
VERSION BX553072.1 GI:33377271
SOURCE EST.
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK

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morsitans morsitans cDNA clone Tse129e08_plc, mRNA sequence.
 BX553451
 VERSION BX553451.1 GI:33377612
 EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 28)
 REFERENCE Lehan, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
 AUTHORS Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehan, S. and Hall, N.
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942
 PUBMED 14519198
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
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 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehan
 Prof. M.J. Lehan
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all plc reads are from
 the 3' end.
 FEATURES
 source
 Location/Qualifiers
 1..28
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse129e08_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"
 Query Match 0.2%; Score 18.6; DB 1; Length 28;
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
 ||| |||||
 Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 28
 RESULT 817
 BX553531
 LOCUS 28 bp mRNA linear EST 10-OCT-2003
 DEFINITION Glossina morsitans morsitans adult infected gut Glossina
 morsitans morsitans cDNA clone Tse12a08_plc, mRNA sequence.
 ACCESSION BX553531
 VERSION BX553531.1 GI:33377683
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 28)
 REFERENCE Lehan, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
 AUTHORS Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehan, S. and Hall, N.
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 response genes
 JOURNAL Genome Biol. 4 (10), R63 (2003)
 MEDLINE 22881942

14519198
 PUBMED
 COMMENT Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehan
 Prof. M.J. Lehan
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all plc reads are from
 the 3' end.
 FEATURES
 source
 Location/Qualifiers
 1..28
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
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 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"
 Query Match 0.2%; Score 18.6; DB 1; Length 28;
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
 ||| |||||
 Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 28
 RESULT 818
 BX553626
 LOCUS 28 bp mRNA linear EST 10-OCT-2003
 DEFINITION Glossina morsitans morsitans adult infected gut Glossina
 morsitans morsitans cDNA clone Tse12f05_plc, mRNA sequence.
 ACCESSION BX553626
 VERSION BX553626.1 GI:33377771
 KEYWORDS EST.
 SOURCE Glossina morsitans morsitans
 ORGANISM Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 28)
 REFERENCE Lehan, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
 AUTHORS Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehan, S. and Hall, N.
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 JOURNAL Genome Biol. 4 (10), R63 (2003)
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 PUBMED 14519198
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 Prof. M.J. Lehan
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW
 All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all plc reads are from
 the 3' end.
 FEATURES
 source
 Location/Qualifiers
 1..28
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse12a08_plc"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"


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Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 824
BX555683
LOCUS BX555683 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse22b11_pic, mRNA sequence.
ACCESSION BX555683
VERSION BX555683.1 GI:33379660
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
source
1..28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse22d02_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 826
BX555881
LOCUS BX555881 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse23e03_pic, mRNA sequence.
ACCESSION BX555881
VERSION BX555881.1 GI:33379851
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
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response genes
Genome Biol. 4 (10), R63 (2003)
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COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 825
BX555705
LOCUS BX555705 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse22d02_pic, mRNA sequence.
ACCESSION BX555705
VERSION BX555705.1 GI:33379682
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```

```

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
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COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
source
1..28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse22d02_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 826
BX555881
LOCUS BX555881 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse23e03_pic, mRNA sequence.
ACCESSION BX555881
VERSION BX555881.1 GI:33379851
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
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morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane

```

School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end

FEATURES

source

Location/Qualifiers

1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse25h07_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 28

RESULT 827

BX556242

LOCUS

DEFINITION

BX556242 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse25h07_plc, mRNA sequence.

ACCESSION

BX556242

VERSION

BX556242.1 GI:33380171

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

REFERENCE

1 (bases 1 to 28)

Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

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Request for clones, please contact: Mike Lehane

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University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all plc reads are from

the 3' end.

Location/Qualifiers

1..28

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse25h07_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Query Match

Best Local Similarity

Matches

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 28

RESULT 828

BX556265

LOCUS

DEFINITION

BX556265 Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tse26a09_plc, mRNA sequence.

ACCESSION

BX556265

VERSION

BX556265.1 GI:33380194

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

REFERENCE

1 (bases 1 to 28)

Lehane, M.J., Aksoy, S., Gibson, W., Kexhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all plc reads are from

the 3' end.

Location/Qualifiers

1..28

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse26a09_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Location/Qualifiers

1..28

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse26a09_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

Location/Qualifiers

1..28

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clone="Tse26a09_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

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VERSION      BX556442.1  GI:33427704
KEYWORDS     EST.
SOURCE       Glossina morsitans morsitans
ORGANISM     Glossina morsitans morsitans
              Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Hippoboscidae; Glossinidae; Glossina.
REFERENCE    1 (bases 1 to 28)
AUTHORS      Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
              Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE        Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J.Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all pic reads are from
              the 3' end.

FEATURES     source
              Location/Qualifiers
                1..28
                /organism="Glossina morsitans morsitans"
                /mol_type="mRNA"
                /sub_species="morsitans"
                /db_xref="taxon:37546"
                /clone="Tse27e04_pic"
                /tissue_type="adult infected gut"
                /clone_lib="Glossina morsitans morsitans adult infected
                gut"
                /note="country: Zimbabwe; EST from adult gut infected with
                T.brucei"

Query Match      0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
      ||| ||||| ||||| ||||| |||||
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 830
BX556491
LOCUS      BX556491 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse27e04_pic, mRNA sequence.
ACCESSION  BX556491
VERSION     BX556491.1 GI:33427752
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
ORGANISM    Glossina morsitans morsitans
              Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Hippoboscidae; Glossinidae; Glossina.
REFERENCE    1 (bases 1 to 28)
AUTHORS      Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
              Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE        Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J.Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all pic reads are from
              the 3' end.

FEATURES     source
              Location/Qualifiers
                1..28
                /organism="Glossina morsitans morsitans"
                /mol_type="mRNA"
                /sub_species="morsitans"
                /db_xref="taxon:37546"
                /clone="Tse27b01_pic"
                /tissue_type="adult infected gut"
                /clone_lib="Glossina morsitans morsitans adult infected
                gut"
                /note="country: Zimbabwe; EST from adult gut infected with
                T.brucei"

Query Match      0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
      ||| ||||| ||||| ||||| |||||
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 830
BX556491
LOCUS      BX556491 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse27e04_pic, mRNA sequence.
ACCESSION  BX556491
VERSION     BX556491.1 GI:33427752
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
ORGANISM    Glossina morsitans morsitans
              Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Hippoboscidae; Glossinidae; Glossina.
REFERENCE    1 (bases 1 to 28)
AUTHORS      Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
              Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE        Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL      Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J.Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all pic reads are from
              the 3' end.

FEATURES     source
              Location/Qualifiers
                1..28
                /organism="Glossina morsitans morsitans"
                /mol_type="mRNA"
                /sub_species="morsitans"
                /db_xref="taxon:37546"

```


Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane

Bangor LL57 20W
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source

Location/Qualifiers

1. .28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse43h11_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 840

BX560221

LOCUS

DEFINITION BX560221 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse48g03_plc, mRNA sequence.

ACCESSION

BX560221

VERSION

BX560221.1

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 28)

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

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response genes

Genome Biol. 4 (10), R63 (2003)

MEDLINE

PUBMED

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 20W

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

Location/Qualifiers

1. .28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse48g03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 841

BX562150

LOCUS

DEFINITION BX562150 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse5a06_plc, mRNA sequence.

ACCESSION

BX562150

VERSION

BX562150.1

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 28)

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

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Genome Biol. 4 (10), R63 (2003)

MEDLINE

PUBMED

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 20W

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

Location/Qualifiers

1. .28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse5a06_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 842

BX562296

LOCUS

DEFINITION BX562296 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse5h05_plc, mRNA sequence.

ACCESSION

BX562296

VERSION

BX562296.1

KEYWORDS

EST.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .20

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF-03-A01"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTTTTTTTTT 4483

Db 1 TTTTGTGTTTTTTTTTTT 20

RESULT 848

A2375620/c

LOCUS

AZ375620 20 bp DNA linear GSS 02-OCT-2000
IM0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0129A08 F, genomic survey sequence.

ACCESSION

A2375620

VERSION

A2375620.1

GI:10489320

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: A column: 08

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 3.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTTTTTTTTT 4483

Db 20 TTTTGTGTTTTTTTTTTT 1

RESULT 849

A2486787

LOCUS

AZ486787 20 bp DNA linear GSS 05-OCT-2000
IM0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315D23 F, genomic survey sequence.

ACCESSION

A2486787

VERSION

A2486787.1

GI:10653904

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 23

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0315D23"

/sex="Male"

FEATURES	source
1. .20	Location/Qualifiers
/organism="Mus musculus"	
/mol_type="genomic DNA"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="UUGC2M0213D24"	
/sex="Female"	
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"	
/clone_lib="Mouse 10kb plasmid UUGC2M library"	
/notes="Vector: PWD42nv; Purified genomic DNA from M."	

FEATURES	Location/Qualifiers
source	1. . 21
	/organism="Glossina morsitans morsitans"
	/mol_type="mRNA"
	/sub_species="morsitans"
	/db_xref="taxon:37546"
	/clone="Tse101903_p1c"
	/tissue_type="adult infected gut"
	/clone_lib="Glossina morsitans morsitans adult infected gut"
	/note="country: Zimbabwe; EST from adult gut infected with


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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTT 4482
      ||||| ||||| ||||| |||||
Db 2 CTTTTCGTTTTTTTTTTT 21

RESULT 857
AZ317208
LOCUS      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION 1M003502R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M003502 R, genomic survey sequence.
ACCESSION  AZ317208
VERSION     AZ317208.1  GI:10365804
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 21)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"

/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0035J02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTT 4483
      ||||| ||||| ||||| |||||
Db 1 TTTTTCGTTTTTTTTTTT 20

RESULT 858
AZ486776
LOCUS      21 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION 1M003510F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M003510 F, genomic survey sequence.
ACCESSION  AZ486776
VERSION     AZ486776.1  GI:10653882
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 21)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 10
Seq primer: CGTTGTAACACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"

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/clone="UUGC2M0156D09"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 21 TTTT TTTT GTTTTT TTTT TTTT TTTT TTTT 2

```

```

RESULT 861
BX556059      22 bp mRNA linear EST 10-OCT-2003
LOCUS      BX556059 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION      morsitans morsitans cDNA clone Tse24f09_plc, mRNA sequence.
ACCESSION      BX556059
VERSION      BX556059.1 GI:33380008
KEYWORDS      EST.
SOURCE      Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 22)
Lehane, M.J., Akcey, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

```

```

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

```

```

FEATURES
source
1..22
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"

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```

/clone="Tse24f09_plc"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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```

Query Match      0.2%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

```

```

RESULT 862
BX590647      23 bp mRNA linear EST 06-DEC-2002
LOCUS      BX590647 S015086-024-018-P17-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION      cDNA clone 024-018-P17 5-PRIME, mRNA sequence.
ACCESSION      BX590647
VERSION      BX590647.1 GI:26120230
KEYWORDS      EST.
SOURCE      Beta vulgaris
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 23)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 23 Std Error: 0.00
Plate: 18 row: P column: 17
Seq primer: SP6; CATACGATTAGTGACACTATAG.

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FEATURES
source
1..23
Location/Qualifiers
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:189468"
/db_xref="taxon:161934"
/clone="024-018-P17"
/tissue type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: PCWVSP0R6; Site: 1; Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kwa.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

```

Query Match      0.2%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      4463 CTTTTTTTTTTTTTTTTT 4482
Db      2 CTTTTTTTTTGTTTTTT 21

RESULT 863
CF290998/c
LOCUS   14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION
ACCESSION CF290998
VERSION   CF290998.1 GI:33660031
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1. .23
CF290998 23 bp mRNA linear EST 14-AUG-2003
14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
CF290998
CF290998.1 GI:33660031
EST.
Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4466 TTTTTTTTTTTTTTTTGTCT 4485
Db      1 TTTTTTTTTTTTTTTTGGT 20

RESULT 865
CF314322
LOCUS   HD--02-M20.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--02-M20, mRNA sequence.
ACCESSION CF314322
VERSION   CF314322.1 GI:33686083
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4468 TTTTTTTTTTTTTTTTGTCT 4487
Db      23 TTTTTTTTTTTTTTTTGGCT 4

RESULT 864
CF291486
LOCUS   14ROOT--01-O21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--01-O21, mRNA sequence.
ACCESSION CF291486
VERSION   CF291486.1 GI:33660519
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

```

```

Query Match      0.2%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTTCTTTTCTTTTCTTTTCTTTT 4483
DB 1 TTTTCTTTTCTTTTCTTTTCTTTTAT 20

RESULT 866
CF333801
LOCUS
DEFINITION JMT--02-N11.g1 AtJMT-overexpressing transgenic rice plasmid CDNA
library (JMT) Oryza sativa CDNA clone JMT--02-N11, mRNA sequence.
ACCESSION CF333801
VERSION CF333801.1 GI:33815910
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 23)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
location/Qualifiers
1..23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-N11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.2%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTTCTTTTCTTTTCTTTTCTTTT 4483
DB 2 TGTCTTTTCTTTTCTTTTCTTTTCTTT 21

RESULT 867
AZ627850/c
LOCUS
DEFINITION IM0474N20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474N20 F, genomic survey sequence.
ACCESSION AZ627850
VERSION AZ627850.1 GI:11750136
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Query Match      0.2%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4463 CTTTCTTTTCTTTTCTTTTCTTTT 4482
DB 20 CTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 868
AZ764519/c
LOCUS
DEFINITION IM0560P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0560P11 R, genomic survey sequence.
ACCESSION AZ764519
VERSION AZ764519.1 GI:12879566
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: N column: 20
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
source
location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474N20"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhauser,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0560 row: P column: 11
Seq primer: CACACGAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0560P11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gil4732114[gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4481
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AATTTTTTTTTTTTTTTTTT 1

RESULT 869
AW333508
LOCUS AW333508 26 bp mRNA linear EST 31-JAN-2000
DEFINITION S22F8 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
ACCESSION AW333508
VERSION AW333508.1 GI:6829865
KEYWORDS EST.
SOURCE
ORGANISM
Pneumocystis carinii
Pneumocystis carinii
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
Pneumocystidaceae; Pneumocystis.
1 (bases 1 to 26)
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
Edman,J.C., Kovacs,J. and Cushion,M.

derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 18.4; DB 1; Length 27;
 Best Local Similarity 95.0%; Pred. No. 6.8e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4467 TTTTTCCTTTTTCCTTCGTC 4486
 |||||
 Db 1 TTTTTCCTTTTTCCTTCATC 20

RESULT 871
 A2514352/c
 LOCUS
 DEFINITION 28 bp DNA linear GSS 05-OCT-2000
 clone UUGC1M0360F06 R, genomic survey sequence.
 ACCESSION A2514352
 VERSION A2514352.1 GI:10695668
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (Bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5605
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0360 row: F column: 06
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 FEATURES
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0360F06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel,
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 28;
 Best Local Similarity 78.6%; Pred. No. 7.3e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 4012 AAAATGAGAAAAAGAGAGAAAAACAAA 4039
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 Db 28 AAAAAGAAAAAAGAAAAAAGAAAAA 1
 RESULT 872
 A2357605
 LOCUS
 DEFINITION 28 bp DNA linear GSS 02-OCT-2000
 clone UUGC1M0099115 F, genomic survey sequence.
 ACCESSION A2357605
 VERSION A2357605.1 GI:10471305
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (Bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.,
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5605
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0099 row: I column: 15
 Seq primer: CGTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 28.
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0099115"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."


```

Query Match      0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4020 AAAAAAGAGAGAAACAAATGTTATTT 4047
      ||||| 1 ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAATTTTTTTT 28

RESULT 873
CF307749/c
LOCUS
DEFINITION ABF--01-E17.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--01-E17, mRNA sequence.
ACCESSION CF307749
VERSION CF307749.1 GI:33679510
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--01-E17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_hosts="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOP0; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGACAGACAAACAAA 4039
      ||||| 1 ||||| ||||| ||||| |||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 874
BX556035
LOCUS
DEFINITION BX556035 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse24e05_pic, mRNA sequence.
ACCESSION BX556035
VERSION BX556035.1 GI:33436165
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES

source

Location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse24e05_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTT 4481

Db 9 AGTTTTTTTTTTTTTTTTTT 28

RESULT 875

BX560649

LOCUS

DEFINITION

BX560649 Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tse50c12_pic, mRNA sequence.

ACCESSION

BX560649

VERSION

BX560649.1 GI:33369590

KEYWORDS

EST.

SOURCE

Glossina morsitans morsitans

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 28)

Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,

Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES

source
1. .28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="rRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="rse50c12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTT 4481

Db 9 AGTTTTTTTTTTTTTTTTTT 28

RESULT 876
A2785111/c
LOCUS A2785111 31 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M002B14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M002B14 R, genomic survey sequence.

ACCESSION A2785111
VERSION A2785111.1 GI:12921525
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: B column: 14

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 31.

Location/Qualifiers

1. .31

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M002B14"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 31;
Best Local Similarity 78.6%; Pred. No. 8.9e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039

Db 30 AAAAAAAAAAAAAAAAAAGAAAAAAAAA 3

RESULT 877

AZ307192

LOCUS

DEFINITION

clone UUGC1M0008B07 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 34)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: B column: 07

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 34.

Location/Qualifiers

1. .34

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0008B07"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers
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 /tissue_type="leaf"
 /dev_stage="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="AJMT-overexpressing transgenic rice plasmid
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 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
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 prepared from Arabidopsis Jaemoinate Carboxyl
 methyltransferase overexpression line."

Query Match
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 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4469 TTTTGTCTTTTGTCTTGAG 4491
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 Db 1 TTTTGTCTTTTGTCTATAG 23

RESULT 881

LOCUS
 DEFINITION
 Yb59h02.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone
 IMAGE:75507 3' similar to gb:M17589 TYROSINE
 3-MONOOXYGENASE ISOZYMES (HUMAN), mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., Dubucque, T., Favello, A., Gish, W.,
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
 Rohlfing, T., Scheillenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
 Travaaekis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
 and Marra, M.

TITLE
 JOURNAL
 MEDLINE
 PUBMED

COMMENT
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 9704478
 8889549
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -21ml3
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:505236"

Query Match
 Best Local Similarity 0.2%; Score 18.2; DB 1; Length 26;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

/db_xref="taxon:9606"
 /clone="IMAGE:75507"
 /sex="female"
 /dev_stage="49 year old"
 /lab_host="SOUR cells (kanamycin resistant)"
 /clone_lib="Stratagene ovary (#937217)"
 /note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
 Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
 Total ovary tissue, normal, caucasian. Average insert
 size: 0.8 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'
 GAATTCGGCAGGAG 3' -3' adaptor sequence: 5'
 CTCGAGGTGTTTTTTTTTTT 3"

Query Match
 Best Local Similarity 0.2%; Score 18.2; DB 1; Length 25;
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4471 TTTTGTCTTTTGTCTTGAGAC 4493
 |||||
 Db 1 TTTTGTCTTTTGTCTTGAGAC 23

RESULT 882

LOCUS
 DEFINITION
 BX560008 Glossina morsitans morsitans adult infected gut Glossina
 morsitans morsitans cDNA clone Tse47c08_p1c, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE

ORGANISM
 Glossina morsitans morsitans
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Hippoboscidae; Glossinidae; Glossina.
 1 (bases 1 to 26)
 Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

REFERENCE

AUTHORS
 TITLE
 Adult midgut expressed sequence tags from the tsetse fly Glossina
 morsitans morsitans and expression analysis of putative immune
 response genes

JOURNAL
 MEDLINE
 PUBMED

COMMENT
 Contact: Hall N
 Pathogen Sequencing Unit
 The Sanger Institute The Wellcome Trust Genome Campus
 Hinxton, Cambridge, CB10 1SA, UK
 Request for clones, please contact: Mike Lehane
 Prof. M.J. Lehane
 School of Biological Sciences,
 University of Wales,
 Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'
 end of the cDNA all p1c reads are from
 the 3' end.

FEATURES

Location/Qualifiers
 1..26
 /organism="Glossina morsitans morsitans"
 /mol_type="mRNA"
 /sub_species="morsitans"
 /db_xref="taxon:37546"
 /clone="Tse47c08_p1c"
 /tissue_type="adult infected gut"
 /clone_lib="Glossina morsitans morsitans adult infected
 gut"
 /note="country: Zimbabwe; EST from adult gut infected with
 T.brucei"

Qy	4459	TGAGACTTTT	TTTTTTTTTTTTTT	4481
Db	4	TAGAAAGTTT	TTTTTTTTTTTTTT	26
RESULT 883				
LOCUS	AZ785554	27 bp	DNA	linear
DEFINITION	2M0029G02R	Mus 10kb plasmid UUGC1M library	Mus musculus	genomic
ACCESSION	AZ785554			
VERSION	AZ785554.1	GI:12922429		
KEYWORDS	GSS.			
SOURCE	Mus musculus	(house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 27)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingley,A., von Niederhausern,A. and Wright,D., Weis,R.			
TITLE	Mus whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0029 row: G column: 02 Seq primer: CACACGGAACACGCTATGACC Class: plasmid ends High quality sequence stop: 27. Location/Qualifiers 1..27 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC2M0029G02" /sex="Male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse 10kb plasmid UUGC1M library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
FEATURES				
source				
Query Match	0.2%	Score 18.2;	DB 1;	Length 27;
Best Local Similarity	87.0%	Pred. No. 7.3e+02;		
Matches	20;	Conservative	0;	Mismatches 3; Indels 0; Gaps 0;
Qy	4464	TTTTTTTTTTTTTTTTTTTT	TTTTTTTGTCTC	4486

RESULT	887
AZ345610	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0080 row: C column: 24
Seq primer: CGTTGTAAAAACGACGGCCAGT

Query Match	4009
Best Local	1
Matches	2

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000) -
Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical
Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801.595.5606

```

Tel: 801 585 5606
Fax: 801 585 7177
Email: dunnm@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: C column: 24
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 34.
Location/Qualifiers
1. 34
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUCG1M0080C24"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

Query/Match      0.2%; Score 18.2; DB 1; Length 34;
Best Local Similarity 74.2%; Pred. NO. 1.1e+03;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4009 TCTAAATTCAGAAAAAGAGAGAAAAACAAAA 4039
      | | | | | | | | | | | | | | | | | |
Db 1 TTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 31
      | | | | | | | | | | | | | | | | | |

```


of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source
1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--03-J04"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 891

CF297446 18 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--08-F02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sativa cDNA clone 30DGS--08-F02, mRNA sequence.

ACCESSION CF297446
VERSION CF297446.1 GI:33666479
KEYWORDS EST.

SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source
1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--08-F02"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 892

CF299027 18 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--02-N14, mRNA sequence.

ACCESSION CF299027

VERSION CF299027.1 GI:33670788

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

FEATURES

source
1. .18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--02-N14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
Db 1 TTTT TTTT TTTT TTTT TTTT 18

RESULT 893

CF299674 18 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--03-M14, mRNA sequence.

ACCESSION CF299674

VERSION CF299674.1 GI:33671435

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

JOURNAL

CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

```

FEATURES
source
Location/Qualifiers
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-03-M14"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match          0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

RESULT 894
CF301325
LOCUS
DEFINITION
7LEAF-06-C12.b1 Rice leaf Plasmid CDNA library II
linear
18 bp mRNA
EST 15-AUG-2003
(7LEAF) Oryza
sativa CDNA clone 7LEAF-06-C12, mRNA sequence.
CF301325
ACCESSION
VERSION
CF301325.1 GI:33673086
KEYWORDS
EST.

SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Angiosperms; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE
AUTHORS
TITLE
JOURNAL

CONTACT: Nehm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES	source
Location/Qualifiers	
1. 18	
/organism="Oryza sativa"	
/mol_type="mRNA"	
/cultivar="Nackdong"	
/db_xref="taxon:4530"	
/clone="7LEAF-06-C12"	
/tissue_type="leaf"	
/dev_stage="7 days after germination"	
/lab_host="E.coli DH10B"	
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"	
/notes="Vector: PCR-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	

Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;

	Matches	18;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	4464	TTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTT	4481						
Db	1	TTTTTTTTTTTTTTTTTTTT	TTTTTTTTTTTTTTTTTTTT	18						

RESULT_895				
CF301760	CF301760	18 bp	mRNA	linear
LOCUS	7LEAF-06-L22.b1	Rice leaf	plasmid	cDNA library II
DEFINITION	sativa cDNA clone 7LEAF-06-L22,	mRNA sequence.		(7LRAF) Oryza
				EST 15-AUG-2003

ACCESSION
 CF301760
 VERSION
 CF301760.1
 KEYWORDS
 GI:33673521
 EST.

SOURCE ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CONTACT
CONTACT: **NAME** : Dr. Bihnam B. Bui
ADDRESS : Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
TEL : 82 31 330 6193
FAX : 82 31 321 6355
E-MAIL : bhnam@bio.myongji.ac.kr

FEATURES source

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-06-L22"
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/dev_stage="7 days after"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf pl"
/notes="Vector: pCR4-TOPO
with oligoribonucleotide
RT-PCR."

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Query Match 0.2%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4481
p'b 1 TTTTTTTTTTTTTTTTTT 18

RESULT 896
CE320418

LOCUS	CF320418	CF320418	18 bp	linear	EST 15-AUG-2003
DEFINITION	HD-11-E22.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)	Orzva sativa cDNA clone HD-11-E22. mRNA sequence.			

ACCESSION
CF320418
VERSION
CF320418.1
KEYWORDS
EST.
GI:33692179

KEYWORDS
SOURCE
ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 18)

AUTHORS	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y.-K. and Nahm, B. H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .18
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD-11-E22"
 /tissue_type="callus"
 /dev_stages="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDA1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

Query Match 0.2%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTT 4480

Db 1 CTTTCTTTTCTTTTCTTTT 18

RESULT 897

CF291665 19 bp mRNA linear EST 14-AUG-2003
 LOCUS 14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza
 DEFINITION sativa cDNA clone 14ROOT--02-D01, mRNA sequence.

ACCESSION CF291665

VERSION CF291665.1 GI:33606098

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="14ROOT--02-D01"
 /tissue_type="root"
 /dev_stages="14 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice root plasmid cDNA library (14ROOT)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTCTTTT 4484

Db 1 TTTTCTTTTCTTTTCTTTT 18

RESULT 898

CF293167 19 bp mRNA linear EST 14-AUG-2003
 LOCUS 30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 DEFINITION sativa cDNA clone 30DGS--02-E02, mRNA sequence.

ACCESSION CF293167

VERSION CF293167.1 GI:33662200

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1. .19
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--02-E02"
 /tissue_type="leaf"
 /dev_stages="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTT 4481

Db 2 TTTTCTTTTCTTTTCTTTT 19

RESULT 899

CF309821 19 bp mRNA linear EST 15-AUG-2003
 LOCUS ABF--04-C17.g1 ABF3-overexpressing transgenic rice plasmid cDNA
 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--04-C17, mRNA sequence.

ACCESSION CF309821

VERSION CF309821.1 GI:33681582

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzeae; Oryza.


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RESULT 905
CF298207/c
LOCUS
DEFINITION 7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-H23, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
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/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TORO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTT 4480
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Db 18 CTTTTTTTTTTTTTTTTT 1

RESULT 906
AZ370699
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DEFINITION 1M0121N17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0121N17 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

RESULT 907
AZ849506/c
LOCUS
DEFINITION 2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

```

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0121 row: N column: 17
Seq primer: CACACAGGAACAGCTATGACC
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High quality sequence stop: 20.
Location/Qualifiers
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/strain="C57BL/6J"
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4481
|||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 907
AZ849506/c
LOCUS
DEFINITION 2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

```

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: P column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

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1..20
Location/Qualifiers
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/clone="UUGC2M0150P21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4464 TTTTITTTTTTTTTTTT 4481

Db 20 TTTTITTTTTTTTTTTT 3

RESULT 908

BX564412

LOCUS

BX564412 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans CDNA clone Tse71e10_p1c, mRNA sequence.

ACCESSION

BX564412

VERSION

BX564412.1

KEYWORDS

EST.

SOURCE

Glossina morsitans morsitans

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.

REFERENCE

1 (bases 1 to 21)

Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

MEDLINE

22881942

PUBMED

14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

FEATURES

source

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1..21
Location/Qualifiers
1..21
/organism="Glossina morsitans morsitans"
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/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse71e10_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

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Query Match      0.2%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4467 TTTTITTTTTTTTTTTT 4484

Db 1 TTTTITTTTTTTTTTTT 18

RESULT 909

AZ943299

LOCUS

AZ943299 21 bp DNA linear GSS 26-APR-2001
2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203K21 R, genomic survey sequence.

ACCESSION

AZ943299

VERSION

AZ943299.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 21)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0203 row: K column: 21

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

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/db_xref="taxon:10090"

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/sex="Female"

/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
 /clone lib="Mouse 10kb plasmid UUGC2M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4463 CTTTTTTTTTTTTTTTTT 4480
 Db 4 CTTTTTTTTTTTTTTTTT 21

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 LOCUS A2843648 22 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0142B07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0142B07 R, genomic survey sequence.

ACCESSION A2843648
 VERSION A2843648.1 GI:13013556
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dduwn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0142 row: B column: 07
 Seq primer: CACACGGAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 22.

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 /strain="C57BL/6J"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4464 TTTTTTTTTTTTTTTTTT 4481
 Db 18 TTTTTTTTTTTTTTTTTT 1

RESULT 911
 TA211D06P
 LOCUS TA211D06P 22 bp DNA linear GSS 13-DEC-2000
 DEFINITION T. brucei sheared genomic DNA clone 211d06, forward sequence,
 genomic survey sequence.

ACCESSION AL478564
 VERSION AL478564.1 GI:11844523
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)

REFERENCE
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.B., Rajandream, M.A. and Barrell, B.G.
 Direct Submission

TITLE
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nleayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
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 /mol_type="genomic DNA"
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 /db_xref="taxon:5691"
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4467 TTTT...TTT 4484
 Db 1 TTTT...TTT 18

RESULT 912
 TA386H07Q 22 bp DNA linear GSS 13-DEC-2000
 T. brucei sheared genomic DNA clone 386H07, reverse sequence,
 genomic survey sequence.

ACCESSION AL498291
 VERSION AL498291.1 GI:11874013
 KEYWORDS GSS.

SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 22)
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrall, B.G.
 Direct Submission
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrall@sanger.ac.uk and
 nh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 Gutrat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrall, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES source
 1..22
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
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 /clone="386H07"

Query Match 0.2%; Score 18; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 4481
 Db 1 TTTT...TTT 18

RESULT 913
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 LOCUS S30G5 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.
 DEFINITION AW334124
 ACCESSION AW334124
 VERSION AW334124.1 GI:6830481
 KEYWORDS EST.

SOURCE Pneumocystis carinii
 ORGANISM Pneumocystis carinii
 Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
 Pneumocystidaceae; Pneumocystis.
 1 (bases 1 to 23)
 Smulian, A.G., Arnold, J., Weise, M., Wunderlich, J., Staben, C.,
 Edman, J.C., Kovacs, J. and Cushion, M.
 Expressed sequence tags from Pneumocystis carinii
 Unpublished (2000)

COMMENT Contact: Staben C
 School of Biological Sciences
 University of Kentucky
 101 Morgan Building, University of Kentucky, Lexington, KY
 40506-0225, USA
 Tel: 606 257 2161
 Fax: 606 257 1717
 Email: staben@pop.uky.edu.

FEATURES source
 1..23
 /organism="Pneumocystis carinii"
 /mol_type="mRNA"
 /db_xref="taxon:4754"
 /lab_host="E. coli"
 /clone_lib="AGS-1"
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 P. carinii organisms (3x10e9) from a single rat (99-1-6,
 sacrificed on 3/17/99) at Cincinnati VA facilities.
 Trizol extracted RNA. Oligo dt priming, standard
 conditions described by vendor, Stratagene. Further
 details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.2%; Score 18; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 4481
 Db 6 TTTT...TTT 23

RESULT 914
 CF293321/c 23 bp mRNA linear EST 14-AUG-2003
 LOCUS 30DGS--02-H12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
 DEFINITION sativa cDNA clone 30DGS--02-H12, mRNA sequence.

ACCESSION CF293321
 VERSION CF293321.1 GI:33662354
 KEYWORDS EST.

SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 23)
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
 Song, S.I., Kim, J.K., Kim, I.-K. and Nahm, B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Gyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
 1..23
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="30DGS--02-H12"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH108"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4481
Db 23 TTTT... 6

RESULT 915
AZ309553/c
LOCUS
DEFINITION
  AZ309553
  1M0016B10F Mouse 10kb plasmid UGCLM library Mus musculus genomic
  Clone UGCLM0016B10 F, genomic survey sequence.
ACCESSION
  AZ309553
VERSION
  AZ309553.1 GI:10350837
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 24)
REFERENCE
  Authors
    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
    Ielam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
    Reilly, M., Rose, R., Stokes, R., Tingey, A., von
    Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
JOURNAL
  Unpublished (2000)
COMMENT
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0016 row: B column: 10
  Seq primer: CGTGTAAACGACGCGCAGT
  Class: plasmid ends
  High quality sequence stop: 24.
  Location/Qualifiers
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      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UGCLM0016B10"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UGCLM library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of PWD42 (g1473214[gB]AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

Query Match 0.2%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULTS 917
BQ585188

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Qy 4464 TTTT... 4481
Db 24 TTTT... 7

RESULT 916
T49097
LOCUS
DEFINITION
  T49097
  yb08h08.s1 Stratagene placenta (#937225) Homo sapiens cDNA clone
  IMAGE:70623 3' similar to gb:X62744 CLASS II
  HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN (HUMAN), mRNA sequence.
ACCESSION
  T49097
VERSION
  T49097.1 GI:650957
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 25)
REFERENCE
  Authors
    Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
    Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
    Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
    Marlis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
    Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, P., Thierry-Mieg, J.,
    Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.
    and Marra, M.
  Generation and analysis of 280,000 human expressed sequence tags
  Genome Res. 6 (9), 807-828 (1996)
  97044478
  8889549
  Other ESTs: yb08h08.r1
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  High quality sequence starts: 1
  High quality sequence stops: 1
  Source: IMAGE Consortium, LLNL
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Trace considered overall poor quality
  Seq primer: -21m13
  High quality sequence stop: 1.
  Location/Qualifiers
    1..25
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="GDB:491520"
      /db_xref="taxon:9606"
      /clone="IMAGE:70623"
      /sex="male"
      /lab_host="SOLR cells (kanamycin resistant)"
      /clone_lib="Stratagene placenta (#937225)"
      /notes="Organ: placenta; vector: pBluescript SK-; Site_1:
      EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
      Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP
      XR Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
      adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

Query Match 0.2%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULTS 917
BQ585188

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LOCUS      BQ585188                26 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION  SD14222-024-001-E10-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
ACCESSION  BQ585188
VERSION    BQ585188.1  GI:26114770
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 26)
AUTHORS   Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.;
            Drungowski,M.; Stahl,D.; Wruck,W.; Menze,A.; O'Brien,J.; Lehrach,H.
            and Radolof,U.
TITLE      Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL    Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
COMMENT    Contact: Weishaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@mpiz-koeln.mpg.de
            Insert Length: 26 Std Error: 0.00
            Plate: 1 row; E column: 10
            Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES   .
            Location/Qualifiers
            1..26
                /organism="Beta vulgaris"
                /mol_type="mRNA"
                /cultivar="KWS2320 (double haploid, monogerm breeding
                line)"
                /db_xref="GABI:181514"
                /db_xref="taxon:161934"
                /clone="024-001-E10"
                /tissue_type="inflorescence"
                /lab_host="EMPH108"
                /clone_lib="MP1Z-ADIS-024-inflorescence"
                /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                cDNA library from sugar beet, library provided by KWS
                Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
                b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                orientation:
                SP6-SalI-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
                Sequencing granted in the context of the GABI-Beet
                project, local PI: Dr. Katharina Schneider, coordinator:
                Prof. Christian Jung; Sequence submission managed by
                RZPB/GABI-Primary database: http://gabi.rzpd.de"
            Query Match      0.2%; Score 18; DB 1; Length 26;
            Best Local Similarity 100.0%; Pred. No. 7.3e+02;
            Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy  4463  CTTTCTTTTCTTTTCTTTT 4480
Db  7  CTTTCTTTTCTTTTCTTTT 24

RESULT 918
LOCUS      AZ465567                27 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION  1M0275C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0275C17 R, genomic survey sequence.
ACCESSION  AZ465567
VERSION    AZ465567.1  GI:10623788
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

AUTHORS

1 (bases 1 to 27)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0275 row: C column: 17

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 27.

FEATURES

source

Location/Qualifiers

1..27

/organism="Mus musculus"

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/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0275C17"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match

Best Local Similarity 80.8%; Pred. No. 7.8e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2861

AGGAAGCAAGGAGGAGGAGTGGG 2886

Db 2 AGGTGGCATGCTGGAGGAGATGGG 27

RESULT 919

LOCUS

DEFINITION

AZ627840 1M0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0474B05 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0474 row: B column: 05
Seq primer: CGTTGTAACACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 21.

FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC1M0474B05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4468 TTTTCTTTTCTTTCTTTCTTT 4488
Db 1 TGTCTTTTCTTTTCTTTCTTT 21

RESULT 920
CF302435/c
LOCUS CF302435 22 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-022.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-022, mRNA sequence.

ACCESSION CF302435
VERSION CF302435.1 GI:33674196
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 22)

AUTHORS Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. K., and Nahm, B. H.

TITLE Large-scale Sequencing Analysis of Rice ESTs Unpublished (2003)

JOURNAL Contact: Nahm B.H.

COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .22
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-022"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site 1: ECORI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 17.8; DB 1; Length 22;
Best Local Similarity 90.5%; Pred. No. 5.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4466 TTTTCTTTTCTTTTCTTTCTTT 4486
Db 22 TTTTCTTTTCTTTTCTTTCTATC 2

RESULT 921
AL048695/c
LOCUS AL048695 23 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp566D063_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp566D063, mRNA sequence.

ACCESSION AL048695
VERSION AL048695.1 GI:4727766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 23)
EST (Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Koehler, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
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1. .23
/organism="Homo sapiens"
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/clone="DKFZp566D063"
/tissue_type="kidney"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/clone_lib="566 (synonym: hfkd2)"
/notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4466 TTTTCTTTTCTTTTCTTTCTTT 4486
Db 23 TTTCTTTTCTTTTCTTTCTGAC 3

RESULT 922
CF300419/c
LOCUS
DEFINITION
7LEAF--04-M22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--04-M22, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
COMMENT
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source
1..23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF-04-M22"
/tissue_type="leaf"
/dev_stages="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7407 CAACATCAGCAGCAGCAGCAG 7427
Db 23 CGAGCTCAGCAGCAGCAGCAG 3

RESULT 923
AZ308447/c
LOCUS
DEFINITION
AZ308447F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0011J24 F, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0011 row: J column: 24
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.

FEATURES

Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0011J24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4461 GACCTTTTTTTTTTTTTTTT 4481
Db 21 GAGTCTTTTTTTTTTTTTTT 1

RESULT 924
TA130G11Q
LOCUS
DEFINITION
TA130G11Q 23 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 130g11, reverse sequence,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
TITLE
Direct Submission
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nleaved@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source
1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="130g11"

Query Match 0.2%; Score 17.8; DB 1; Length 23;
Best Local Similarity 90.5%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 2;

QY 3726 CATTCATTGAGCTTTTAAAA 3746

Db 3 CATTTATTGTGCTTTTAAAA 23

RESULT 925

LOCUS BX621433/c
DEFINITION BX621433 NAPI Anopheles gambiae cDNA clone ANGNP111A03T7, mRNA sequence.

ACCESSION BX621433

VERSION BX621433.1 GI:33542952

KEYWORDS

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

REFERENCE

1 (bases 1 to 24)
Lobo,N.L., Gardner,M., Romans,P. and Collins,P.H.

Authors Anopheles gambiae EST, Center for Tropical Disease Research and Training

JOURNAL

COMMENT Contact: Frank H. Collins
Center for Tropical Disease Research and Training

University of Notre Dame

Notre Dame, IN 46556, USA

Tel: 574-631-9245

Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

FEATURES

source
1. .24
/organism="Anopheles gambiae"
/mol_type="mRNA"
/db_xref="taxon:7165"
/clone="ANGNP111A03T7"
/lab_host="E. coli DH10B"
/clone_lib="NAPI"
/note="Vector: p7T3D-Pac (Pharmacia); Site 1: NotI;
Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAPI is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

Query Match 0.2%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7410 CATCAGCAGCAGCAGCAGCAG 7430

Db 22 CGTCAGCAGCAGCAGCAGCAG 2

RESULT 926

AZ486450

LOCUS

DEFINITION

AZ486450 24 bp DNA linear GSS 05-OCT-2000

clone UUGC1M0314A06 R, genomic survey sequence.

ACCESSION AZ486450

VERSION AZ486450.1 GI:10653235

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 24)
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., fingley,A., von

Niederhauser,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0314 row: A column: 06

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

Location/Qualifiers

1. .24

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0314A06"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv, Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gil4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 24;

Best Local Similarity 90.5%; Pred. No. 6.6e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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QY 6986 ACAGATGAGTGGGAAAGGG 7006
DB 3 AGAGATGGGTGGGAAAGGG 23

RESULT 927
AZ814559
LOCUS 24 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0082P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0082P18 F, genomic survey sequence.
ACCESSION AZ814559
VERSION AZ814559.1 GI:12984467
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2010 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: P column: 18
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
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1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTTTT 4483
DB 22 CTTTTTTTGTGTTTTTAAT 2

RESULT 929
BX554728
LOCUS 26 bp mRNA linear EST 10-OCT-2003
DEFINITION BX554728 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse17b03_plc, mRNA sequence.
ACCESSION BX554728.1 GI:33436050
VERSION EST.
KEYWORDS Glossina morsitans morsitans
SOURCE Glossina morsitans morsitans
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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DB 4 CTTTTTTTCTTTCTTTTTT 24

RESULT 928
AI445764
LOCUS 25 bp mRNA linear EST 13-APR-1999
DEFINITION tJ09G10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2141058 3,
similar to SW1M04 PARTE P15605 HYPOTHETICAL 18.8 KD PROTEIN
; contains element L1 repetitive element ;, mRNA sequence.
ACCESSION AI445764
VERSION AI445764.1 GI:4290493
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 715 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
FEATURES
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1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2141058"
/tissue="poorly differentiated adenocarcinoma with
signal ring cell features"
/lab_host="DH10B"
/clone_lib="NCI-CGAP Gas4"
/notes="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 7.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTTTT 4483
DB 22 CTTTTTTTGTGTTTTTAAT 2

RESULT 929
BX554728
LOCUS 26 bp mRNA linear EST 10-OCT-2003
DEFINITION BX554728 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse17b03_plc, mRNA sequence.
ACCESSION BX554728.1 GI:33436050
VERSION EST.
KEYWORDS Glossina morsitans morsitans
SOURCE Glossina morsitans morsitans
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

```

Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 26)

Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

CONTACT: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES

source

1. .26

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clones="Tse17b03_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.8; DB 1; Length 26;

Best Local Similarity 86.4%; Pred. No. 7.8e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4483

Db 5 ANATGTTTTTCTTTTCTTTTCTTTTCTTTT 26

RESULT 930

BX555158

LOCUS

DEFINITION BX555158 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse19h01_plc, mRNA sequence.

ACCESSION BX555158

VERSION BX555158.1 GI:33379177

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

CONTACT: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES

source

1. .27

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clones="Tse19h01_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 17.8; DB 1; Length 27;

Best Local Similarity 90.5%; Pred. No. 8.4e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4458 ATGACTTTTCTTTTCTTTTCTTTT 4478

Db 7 ATGGTTTTTCTTTTCTTTTCTTTTCTTTT 27

RESULT 931

BX560069

LOCUS

DEFINITION BX560069 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse47g08_plc, mRNA sequence.

ACCESSION BX560069

VERSION BX560069.1 GI:33368106

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

CONTACT: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

FEATURES

source

1. .27

/organism="Glossina morsitans morsitans"

/mol_type="mRNA"

/sub_species="morsitans"

/db_xref="taxon:37546"

/clones="Tse47g08_plc"

/tissue_type="adult infected gut"

/clone_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Reilly,M., Rose,M., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: F column: 17
Seq primer: CGTGTAAACAGCGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

FEATURES

source

1. .29
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0103F17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 29;
Best Local Similarity 75.9%; Pred. No. 9.6e+02;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAAGAGAGAAAAACAAAAT 4040
||||| ||||| ||||| ||||| |||||
Db 29 AAAACACAAAAAACAACAAAAAATAAT 1

RESULT 935

AZ597046

LOCUS

DEFINITION AZ597046 31 bp DNA linear GSS 13-DEC-2000
clone UUGC1M0410K08 R, genomic survey sequence.

ACCESSION AZ597046

VERSION AZ597046.1 GI:11719236

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 31)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von

TITLE

JOURNAL

COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0410 row: K column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.
Location/Qualifiers
1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0410K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

FEATURES

source

1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0410K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 31;
Best Local Similarity 75.9%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAAGAGAGAAAAACAAAAT 4040
||||| ||||| ||||| ||||| |||||
Db 3 AAAACACAAAAAACAACAAAAAATAAT 31

RESULT 936

AZ400441

LOCUS

DEFINITION

AZ400441 32 bp DNA linear GSS 03-OCT-2000

clone UUGC1M0166C14 R, genomic survey sequence.

ACCESSION AZ400441

VERSION AZ400441.1 GI:10515515

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 32)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: C column: 14
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.

FEATURES

source	Location/Qualifiers
1..32	/organism="Mus musculus"
	/mol_type="genomic DNA"
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	/clone="UUGCIW0166C14"
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	/clone_lib="Mouse 10kb plasmid UUGCIM library"
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114.gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.28; Score 17.8; DB 1; Length 32;
Best Local Similarity 75.9%; Pred. No. 1.e+03;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY - 4012 AAAATGAGAAAAAAGAGAGAAAACMAAT 4040
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DB 3 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAT 31

RESULT 937
AL587609/c
LOCUS AL587609 BP Chicken Brain Library Gallus gallus cdna clone
DEFINITION ROS059GG05, mRNA sequence.
ACCESSION AL587609
VERSION AL587609.1 GI:13192643
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 33)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray

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Db      33 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 939
LOCUS   AL587876/c
DEFINITION BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION AL587876
VERSION   AL587876.1 GI:13192910
KEYWORDS EST.
SOURCE   Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
TITLE     Phasianinae; Gallus.
JOURNAL   1 (bases 1 to 34)
COMMENT   BP Chicken Brain Library
          Contact: Frazer Murray
          Dept. Genomics and Bioinformatics
          Roslin Institute
          Roslin, Midlothian, EH25 9PS, UK
          Tel: +44 (0)131 527 4200
          Fax: +44 (0)131 440 0434
          Email: frazer.murray@bbsrc.ac.uk
          GCGGCGCGCTTTTTCCTTTTTCCTTTT 3' Poly A RNA purchased from Clontech
          (*6854-
          Seq primer: M13F.
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            1..34
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              GCGGCGCTTTTTCCTTTTTCCTTTT 3' Poly A RNA purchased from
              Clontech (*6854-1)"

FEATURES             source
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Best Local Similarity 75.9%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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RESULT 940
LOCUS   BI094838
DEFINITION EST-CD34N-038 cDNA library of human CD 34+ stem/progenitor cells
ACCESSION BI094838
VERSION   BI094838.1 GI:17737215
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE     1 (bases 1 to 24)
          Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
          The pattern of gene expression in human hematopoietic CD34+
          stem/progenitor cells
          Unpublished (2001)
          Contact: Wang SM

FEATURES             source
Query Match          0.2%; Score 17.6; DB 1; Length 34;
Best Local Similarity 75.9%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4012 AAATGAGAAAAGAGAGAAAACAAAT 4040
        ||||| ||||| ||||| ||||| |||||
Db      29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 940
LOCUS   BI094838
DEFINITION EST-CD34N-038 cDNA library of human CD 34+ stem/progenitor cells
ACCESSION BI094838
VERSION   BI094838.1 GI:17737215
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE     1 (bases 1 to 24)
          Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
          The pattern of gene expression in human hematopoietic CD34+
          stem/progenitor cells
          Unpublished (2001)
          Contact: Wang SM

FEATURES             source
Query Match          0.2%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4466 TTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTG 4489
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Db      1 TTTTTCCTTTTTCCTTTTTCCTTTTCATG 24

RESULT 941
LOCUS   AZ827015
DEFINITION 2M0103J11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
ACCESSION AZ827015
VERSION   AZ827015.1 GI:12996923
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausen,A. and Wright,D., Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0103 row: J column: 11
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          Class: plasmid ends
          High quality sequence stop: 24.
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              /clone="UUGC2M0103J11"

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Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
Email: swangl@midway.uchicago.edu
This EST fragment was amplified from cDNA Library of human CD 34+ stem/progenitor cells with GLGI technique (Generation of Longer cDNA fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till the first CATG site of the target cDNA sequence.
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
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/tissue_type="Bone marrow"
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/note="3'ESTs converted from the SAGE tag sequences using GLGI method"

Query Match 0.2%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 4466 TTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTG 4489
||||| ||||| ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTTCATG 24

RESULT 941
LOCUS AZ827015
DEFINITION 2M0103J11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
ACCESSION AZ827015
VERSION AZ827015.1 GI:12996923
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D., Weiss,R.
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plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
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84112, USA
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Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
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